SEQUENCE LISTING

SEQ ID NO:1

cDNA sequence of *FIE1*.

SEQ ID NO:2

Amino acid sequence of FIE1.

SEQ ID NO:3

cDNA sequence of *FIE3*.

SEQ ID NO:4

Amino acid sequence FIE3.

SEQ ID NO:5

Genomic sequence of *FIE3*.

SEQ ID NO:6

Genomic sequence of *FIE1*.

Seq. ID No: 1
Seq. ID No: 2

Sequence Size : 2136
Sequence Position: 1 - 2136

Translation Position: 1 - 2136;

Genetic Code : Universal

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        10        20        30        40        50        60        70        80        90       100
AACATCAGAGAAGACGAGAAAAAAAGAAGAGGCGACTGGTTAATGGAGAAGGAAAACCATGAGGACGATGGTGAGGGTTTGCCACCCGAACTAAATCAGA
                                           M  E  K  E  N  H  E  D  D  G  E  G  L  P  P  E  L  N  Q  I

       110       120       130       140       150       160       170       180       190       200
TAAAAGAGCAAATCGAAAAGGAGAGATTTCTGCATATCAAGAGAAAATTCGAGCTGAGATACATTCCAAGTGTGGCTACTCATGCTTCACACCATCAATC
  K  E  Q  I  E  K  E  R  F  L  H  I  K  R  K  F  E  L  R  Y  I  P  S  V  A  T  H  A  S  H  H  Q  S

       210       220       230       240       250       260       270       280       290       300
GTTTGACTTAAACCAGCCCGCTGCAGAAGATGATAATGGAGGAGACAACAAATCACTTTTGTCGAGAATGCAAAACCCACTTCGTCATTTCAGTGCCTCA
 F  D  L  N  Q  P  A  A  E  D  D  N  G  G  D  N  K  S  L  L  S  R  M  Q  N  P  L  R  H  F  S  A  S

       310       320       330       340       350       360       370       380       390       400
TCTGATTATAATTCTTACGAAGATCAAGGTTATGTTCTTGATGAGGATCAAGATTATGCTCTTGAAGAAGATGTACCATTATTTCTTGATGAAGATGTAC
S  D  Y  N  S  Y  E  D  Q  G  Y  V  L  D  E  D  Q  D  Y  A  L  E  E  D  V  P  L  F  L  D  E  D  V  P

       410       420       430       440       450       460       470       480       490       500
CATTATTACCAAGTGTCAAGCTTCCAATTGTTGAGAAGCTACCACGATCTATTACATGGGTCTTCACCAAAAGTAGCCAGCTGATGGCTGAAAGTGATTC
  L  L  P  S  V  K  L  P  I  V  E  K  L  P  R  S  I  T  W  V  F  T  K  S  S  Q  L  M  A  E  S  D  S

       510       520       530       540       550       560       570       580       590       600
TGTGATTGGTAAGAGACAAATCTATTATTTGAATGGTGAGGCACTAGAATTGAGCAGTGAAGAAGATGAGGAAGATGAAGAAGAAGATGAGGAAGAAATC
 V  I  G  K  R  Q  I  Y  Y  L  N  G  E  A  L  E  L  S  S  E  E  D  E  E  D  E  E  E  D  E  E  E  I

       610       620       630       640       650       660       670       680       690       700
AAGAAAGAAAAATGCGAATTTTCTGAAGATGTAGACCGATTTATATGGACGGTTGGGCAGGACTATGGTTTGGATGATCTGGTCGTACGGCGTGCTCTCG
K  K  E  K  C  E  F  S  E  D  V  D  R  F  I  W  T  V  G  Q  D  Y  G  L  D  D  L  V  V  R  R  A  L  A

       710       720       730       740       750       760       770       780       790       800
CCAAGTACCTCGAAGTGGATGTTTCGGACATATTGGAAAGATACAATGAACTCAAGCTTGAGAATGATGGATACGCTGGTGAGGCTTCTGATTTGACATC
  K  Y  L  E  V  D  V  S  D  I  L  E  R  Y  N  E  L  K  L  E  N  D  G  Y  A  G  E  A  S  D  L  T  S

       810       820       830       840       850       860       870       880       890       900
CGAGACAATAACTACTGCTTTTCAGGATTTTGCTGATAGACGTCATTGCCGTCGTTGCATGATATTCGATTGTCATAATCATGAGAAGTATGAGCCCGAG
 E  T  I  T  T  A  F  Q  D  F  A  D  R  R  H  C  R  R  C  M  I  F  D  C  H  N  H  E  K  Y  E  P  E

       910       920       930       940       950       960       970       980       990      1000
TCTAGATCCAGCGAAGACAAATCTAGTTTGTTTGAGGATGAAGATAGACAACCATGCAGTGAGCATTGTTACCTCAAGGTGAGGAGTGTGACAGAAGCTG
S  R  S  S  E  D  K  S  S  L  F  E  D  E  D  R  Q  P  C  S  E  H  C  Y  L  K  V  R  S  V  T  E  A  D

      1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
ATCATGTGATGGATAATGATAACTCTATATCAAACAAGATTGTGGTCTCAGATCCAAACAACACTATGTGGACGCCTGTAGAGAAGGATCTTTACTTGAA
  H  V  M  D  N  D  N  S  I  S  N  K  I  V  V  S  D  P  N  N  T  M  W  T  P  V  E  K  D  L  Y  L  K

      1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
AGGAATTGAGATATTTGGCAGAAACAGTTGTGATGTTGCATTAAACATACTTCGGGGCTTAAAGACGTGCCTAGAGATTTACAATTACATGCGCGAACAA
 G  I  E  I  F  G  R  N  S  C  D  V  A  L  N  I  L  R  G  L  K  T  C  L  E  I  Y  N  Y  M  R  E  Q

      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
GATCAATGTACTCATAGTCTAGACCTTAACAAAACTACACAAAGACACAATCAGGTTACCAAAAAAGTATCTCGAAAAAGTAGTAGGTCGGTCCGCAAAA
D  Q  C  T  H  S  L  D  L  N  K  T  T  Q  R  H  N  Q  V  T  K  K  V  S  R  K  S  S  R  S  V  R  K  K

      1310      1320      1330      1340      1350      1360      1370      1380      1390      1400
AATCGAGACTCCGAAAATATGCTCGTTATCCGCCTGCTTTAAAGAAAACAACTAGTGGAGAAGCTAAGTTTTATAAGCACTACACACCATGCACTTGCAA
  S  R  L  R  K  Y  A  R  Y  P  P  A  L  K  K  T  T  S  G  E  A  K  F  Y  K  H  Y  T  P  C  T  C  K

      1410      1420      1430      1440      1450      1460      1470      1480      1490      1500
GTCAAAATGTGGACAGCAATGCCCTTGTTTAACTCACGAAAATTGCTGCGAGAAATATTGCGGGTGCTCAAAGGATTGCAACAATCGCTTTGGCGGATGT
 S  K  C  G  Q  Q  C  P  C  L  T  H  E  N  C  C  E  K  Y  C  G  C  S  K  D  C  N  N  R  F  G  G  C

      1510      1520      1530      1540      1550      1560      1570      1580      1590      1600
AATTGTGCAATTGGCCAATGCACAAATCGACAATGTCCTTGTTTTGCTGCTAATCGTGAATGCGATCCAGATCTTTGTCGGAGTTGTCCTCTTAGCTGTG
N  C  A  I  G  Q  C  T  N  R  Q  C  P  C  F  A  A  N  R  E  C  D  P  D  L  C  R  S  C  P  L  S  C  G

      1610      1620      1630      1640      1650      1660      1670      1680      1690      1700
GAGATGGCACTCTTGGTGAGACACCAGTGCAAATCCAATGCAAGAACATGCAATTCCTCCTTCAAACCCATAAAAAGATTCTCATTGGAAAGTCTGATGT
  D  G  T  L  G  E  T  P  V  Q  I  Q  C  K  N  M  Q  F  L  L  Q  T  H  K  K  I  L  I  G  K  S  D  V

      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800
TCATGGATGGGGTGCATTTACATGGGACTCTCTTAAAAAGAATGAGTATCTCGGAGAATATACTGGAGAACTGATCACTCATGATGAAGCTAATGAGCGT
 H  G  W  G  A  F  T  W  D  S  L  K  K  N  E  Y  L  G  E  Y  T  G  E  L  I  T  H  D  E  A  N  E  R

      1810      1820      1830      1840      1850      1860      1870      1880      1890      1900
GGGAGAATAGAAGATCGGATTGGTTCTTCCTACCTCTTTACCTTGAATGATCAGCTCGAAATCGATGCTCGCCGTAAGGGAAACGAGTTCAAATTTCTCA
G  R  I  E  D  R  I  G  S  S  Y  L  F  T  L  N  D  Q  L  E  I  D  A  R  R  K  G  N  E  F  K  F  L  N

      1910      1920      1930      1940      1950      1960      1970      1980      1990      2000
ATCACTCAGCAAGACCTAACTGCTACGCCAAGTTGATGATTGTGAGAGGAGATCAGAGGATTGGTCTATTTGCGGAGAGAGCAATCGAAGAAGGTGAGGA
  H  S  A  R  P  N  C  Y  A  K  L  M  I  V  R  G  D  Q  R  I  G  L  F  A  E  R  A  I  E  E  G  E  E

      2010      2020      2030      2040      2050      2060      2070      2080      2090      2100
GCTTTTCTTCGACTACTGCTATGGACCAGAACATGCCGACTGGTCCCGTGGTCGAGAACCTAGAAAGACTGGTGCTTCTAAAAGGTCTAAGGAAGCCCGT
 L  F  F  D  Y  C  Y  G  P  E  H  A  D  W  S  R  G  R  E  P  R  K  T  G  A  S  K  R  S  K  E  A  R

      2110      2120      2130      2140
CCAGCTCGTTAGTTTTTGATCTGAGGAGAAGCAGCA
P  A  R  *
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SEQ ID NO:3

AAAGGTGAGTTGTGTGTTGTGTCAGGTCCAAAATAAAAGTTTGTCGTGAGGTCA
AAATCTACGGTTACAGTAATTTTAATAACCTGTGAATCTGTGTCTAATCGAAAAT
TACAAAACACCAGTTGTTGTTGCATGAGAGACTTGTGAGCTTAGATTAGTGTGCG
AGAGTCAGACAGAGAGAGAGATTTCGAATATCGAATGTCGAAGATAACCTTAGG
GAACGAGTCAATAGTTGGGTCTTTGACTCCATCGAATAAGAAATCGTACAAAGT
GACGAATAGGATTCAGGAAGGGAAGAAACCTTTGTATGCTGTTGTTTTCAACTTC
CTTGATGCTCGTTTCTTCGATGTCTTCGTTACCGCTGGTGGAAATCGGATTACTCT
GTACAATTGTCTCGGAGATGGTGCCATATCAGCATTGCAATCCTATGCTGATGAA
GATAAGGAAGAGTCGTTTTACACGGTAAGTTGGGCGTGTGGCGTTAATGGGAAC
CCATATGTTGCGGCTGGAGGAGTAAAAGGTATAATCCGAGTCATTGACGTCAAC
AGTGAAACGATTCATAAGAGTCTTGTGGGTCATGGAGATTCAGTGAACGAAATC
AGGACACAACCTTTAAAACCTCAACTTGTGATTACTGCTAGCAAGGATGAATCT
GTTCGTTTGTGGAATGTTGAAACTGGGATATGTATTTTGATATTTGCTGGAGCTG
GAGGTCATCGCTATGAAGTTCTAAGTGTGGATTTTCATCCGTCTGATATTTACCG
CTTTGCTAGTTGTGGTATGGACACCACTATTAAAATATGGTCAATGAAAGAGTTT
TGGACGTACGTCGAGAAGTCATTCACATGGACTGATGATCCATCAAAATTCCCC
ACAAAATTTGTCCAATTCCCTGTATTTACAGCTTCCATTCATACAAATTATGTAG
ATTGTAACCGTTGGTTTGGTGATTTTATCCTCTCAAAGAGTGTGGACAACGAGAT
CCTGTTGTGGGAACCACAACTGAAAGAGAATTCTCCTGGCGAGGGAGCTTCAGA
TGTTCTATTAAGATACCCGGTTCCAATGTGTGATATTTGGTTTATCAAGTTTTCTT
GTGACCTCCATTTAAGTTCTGTTGCGATAGGTAATCAGGAAGGAAAGGTTTATGT
CTGGGATTTGAAAAGTTGCCCTCCTGTTTTGATTACAAAGTTATCACACAATCAA
TCAAAGTCTGTAATCAGGCAAACAGCCATGTCTGTCGATGGAAGCACGATTCTT
GCTTGCTGCGAGGACGGGACTATATGGCGCTGGGACGTGATTACCAAGTAGCGG
TCTGAGTCTTGTAGGAATTGATGAATTAGGAGTGCGAAGAAATGAGATATCCAT
TCTTTTATTGTAATTCTGATCATGTTGCTACTCCCTGAGACCTTGAGATGCTCTTT
GTAGCCTTGTTAACGTCCACCCTTGTACCACAGTGTATACCCTTTCTGGAGATTT
TGTCTTATTCTCTTAGTTCAATACACAAGGCTGTATCCTGGAGCTTTATTGCAGG
AACCACTCTCTTTCATAAGCTTTCTAGTATTC

SEQ ID NO:4

MSKITLGNESIVGSLTPSNKKSYKVTNRIQEGKKPLYAVVFNFLDARFFDVFV
TAGGNRITLYNCLGDGAISALQSYADEDKEESFYTVSWACGVNGNPYVAAGGV
KGIIRVIDVNSETIHKSLVGHGDSVNEIRTQPLKPQLVITASKDESVRLWNVE
TGICILIFAGAGGHRYEVLSVDFHPSDIYRFASCGMDTTIKIWSMKEFWTYVE
KSFTWTDDPSKFPTKFVQFPVFTASIHTNYVDCNRWFGDFILSKSVDNEILLW
EPQLKENSPGEGASDVLLRYPVPMCDIWFIKFSCDLHLSSVAIGNQEGKVYVW
DLKSCPPVLITKLSHNQSKSVIRQTAMSVDGSTILACCEDGTIWRWDVITK.

Seq. ID No: 5


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10 20 30 40 50 60 70 80 90 100 110 120
TCTGAAGCAGCTAATCGATCCACTAATCTTGTGGAGATCGTGTGTTGCTTTGGTGCATATATATACAAATAGACAAATACATATGCGTTTACATATATATGTAAGCACGTATTTAGAGAGCAA
fle3lond5's/n.seq(1>5801) -> TCTGAAGCAGCTAATCGATCCACTAATCTTGTGGAGATCGTGTGTTGCTTTGGTGCATATATATACAAATAGACAAATACATATGCGTTTACATATATATGTAAGCACGTATTTAGAGAGCAA

130 140 150 160 170 180 190 200 210 220 230 240
CAATAAGGCATGAGAAATGTGATTATCGTCAAATCATGATTGCTACATGACAAATCGATCTTAATTTTGAAAAAGAGACATTTAAATATTCAAAAAACGGTAAAAATTTCTTTAAGACCAACC
fle3lond5's/n.seq(1>5801) -> CAATAAGGCATGAGAAATGTGATTATCGTCAAATCATGATTGCTACATGACAAATCGATCTTAATTTTGAAAAAGAGACATTTAAATATTCAAAAAACGGTAAAAATTTCTTTAAGACCAACC

250 260 270 280 290 300 310 320 330 340 350 360
ATGGAAATAACATGAGAAGACTGAGAGGGAGATTAGAACTTACAACAAGAGAATCTTTTTCCTTCAATATTTTTTTTAAACACTTTTCTTTTGTAGGGAATTTGATAATATGAAATGGATAGA
fle3lond5's/n.seq(1>5801) -> ATGGAAATAACATGAGAAGACTGAGAGGGAGATTAGAACTTACAACAAGAGAATCTTTTTCCTTCAATATTTTTTTTAAACACTTTTCTTTTGTAGGGAATTTGATAATATGAAATGGATAGA

370 380 390 400 410 420 430 440 450 460 470 480 490
TTTTACTGCTTAATTTTTAATCATTTTTTATCAGAAACTTTTTCGTTTTAAATCTACGGCTAGAATTTTCGGTCGGTTTTATACTTTATATAGATGCTAGATTTTTTTCTTCTAGTCATCGTT
fle3lond5's/n.seq(1>5801) -> TTTTACTGCTTAATTTTTAATCATTTTTTATCAGAAACTTTTTCGTTTTAAATCTACGGCTAGAATTTTCGGTCGGTTTTATACTTTATATAGATGCTAGATTTTTTTCTTCTAGTCATCGTT

500 510 520 530 540 550 560 570 580 590 600 610
TATTAGTACAATTTTGTTTTTATATATTGATTACTTGAATTTATAATAGGATTGGTACAAAGGTGGTAATTATAAAGTGCATTTTTTTGGATATTGTTCAATTCAAATATTTTTACTTAGATT
fle3lond5's/n.seq(1>5801) -> TATTAGTACAATTTTGTTTTTATATATTGATTACTTGAATTTATAATAGGATTGGTACAAAGGTGGTAATTATAAAGTGCATTTTTTTGGATATTGTTCAATTCAAATATTTTTACTTAGATT

620 630 640 650 660 670 680 690 700 710 720 730
CTCAAACTATTGAAAAATATCCAAAATATCCGGAAAATTTCAATTTAATCGAATAAAAAAATTAGAATGGAAAGAATAAAAAATTATCGGGTACAATTAGAAGAGTAATGTGTTTAGTTTGGT
fle3lond5's/n.seq(1>5801) -> CTCAAACTATTGAAAAATATCCAAAATATCCGGAAAATTTCAATTTAATCGAATAAAAAAATTAGAATGGAAAGAATAAAAAATTATCGGGTACAATTAGAAGAGTAATGTGTTTAGTTTGGT

740 750 760 770 780 790 800 810 820 830 840 850 860
TTTTACTCGGATACCAGTTCAGTTTTCACGTATTATTCGATCCTATAGGAGCAATTGTGAATTAGTTGTGAGATTTTGGGAGCATTCGCTTCCAGAACTTAGTGCTAGGAGAAATGCTATTTT
fle3lond5's/n.seq(1>5801) -> TTTTACTCGGATACCAGTTCAGTTTTCACGTATTATTCGATCCTATAGGAGCAATTGTGAATTAGTTGTGAGATTTTGGGAGCATTCGCTTCCAGAACTTAGTGCTAGGAGAAATGCTATTTT

870 880 890 900 910 920 930 940 950 960 970 980
CCTATAAGAGTTGTACGAGGAAGCGAGCAAGTACACAACAACCACAAAAGCTTTCAATACTTGTTTACTCCTAGGGTTTAAAACTAGAGGTTCTATAGATCTCTAAATTTTTTTGAACAAATG
fle3lond5's/n.seq(1>5801) -> CCTATAAGAGTTGTACGAGGAAGCGAGCAAGTACACAACAACCACAAAAGCTTTCAATACTTGTTTACTCCTAGGGTTTAAAACTAGAGGTTCTATAGATCTCTAAATTTTTTTGAACAAATG

990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
TGTTTTCCACACGTGATATTCTACAATACCACTCGAAAATTATCCATAATTGCTTTAAACTATTTTTTTGTTTAAATTATATAATTTGTACCGTTGTAAACTGATTATTTCAAATTATAATTA
fle3lond5's/n.seq(1>5801) -> TGTTTTCCACACGTGATATTCTACAATACCACTCGAAAATTATCCATAATTGCTTTAAACTATTTTTTTGTTTAAATTATATAATTTGTACCGTTGTAAACTGATTATTTCAAATTATAATTA

1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 123
AAGCACTATAATTTCATATATTACATTCAACATATATTAAAATAAACTATAACCATGTATTTTTTTGTCTTCCTTTCCTATAAACATTGATTGGACTCTATCGTAAATTTTGTCGTTATCGCA
fle3lond5's/n.seq(1>5801) -> AAGCACTATAATTTCATATATTACATTCAACATATATTAAAATAAACTATAACCATGTATTTTTTTGTCTTCCTTTCCTATAAACATTGATTGGACTCTATCGTAAATTTTGTCGTTATCGCA

1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350
AATTTTGTCGTTATCGATGAGTTTCTCAAAGTTTGGACCTTGATTATCTTGTTTGGAGATGTTCAAATCGTTATATCCAAATAGTGAACTTCTAATTTTCTTTTTTGATAATGTGACTTATTT
fle3lond5's/n.seq(1>5801) -> AATTTTGTCGTTATCGATGAGTTTCTCAAAGTTTGGACCTTGATTATCTTGTTTGGAGATGTTCAAATCGTTATATCCAAATAGTGAACTTCTAATTTTCTTTTTTGATAATGTGACTTATTT

1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470
GGAAAAGTATTCCAAAGTATTCAAATAAACCCTTTAAAAATCCATTAAATACATTTTAAATAAGTAAAATGCTCTCAACGAAGAGATATCATGGTAAATAACAACAGTGAGAGGATAAAATGT
fle3lond5's/n.seq(1>5801) -> GGAAAAGTATTCCAAAGTATTCAAATAAACCCTTTAAAAATCCATTAAATACATTTTAAATAAGTAAAATGCTCTCAACGAAGAGATATCATGGTAAATAACAACAGTGAGAGGATAAAATGT
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        1480      1490      1500      1510      1520      1530      1540      1550      1560      1570      1580      1590
        TAAATCAATTTATTTACAACTTCAAATAGGCGGACATCAAACCTACTTAGCACACTTTCTATTTTCAAATTGGTTATGGTTTGTCTATTAGTTGTTGCATCTATGTTTTTTAATTCTTATATC
fle3lond5's/n.seq(1>5801) -> TAAATCAATTTATTTACAACTTCAAATAGGCGGACATCAAACCTACTTAGCACACTTTCTATTTTCAAATTGGTTATGGTTTGTCTATTAGTTGTTGCATCTATGTTTTTTAATTCTTATATC
Nir Cla-T3(1>23)          ->                               GGCGGACATCAAACCTACTTAGC

        1600      1610      1620      1630      1640      1650      1660      1670      1680      1690      1700      1710      1720
        GGTGATCTTGATTTTGTTTTGGTGTATCTAAAATCTATTTTAGTTAAAGTGCAAGAAAATAAAATAAAAACTTAAGGTAAGAGATGAAAGTAAGCTTTAAATAAAACAGAGCACTTCTATGGT
fle3lond5's/n.seq(1>5801) -> GGTGATCTTGATTTTGTTTTGGTGTATCTAAAATCTATTTTAGTTAAAGTGCAAGAAAATAAAATAAAAACTTAAGGTAAGAGATGAAAGTAAGCTTTAAATAAAACAGAGCACTTCTATGGT

        1730      1740      1750      1760      1770      1780      1790      1800      1810      1820      1830      1840
        CGATTATAGAGCCAAGTTCGTTCCTCCATTTTGGCTTAATGCAATATTACAAGTAAATCTTATAAAACTTTCCATAAGTATCGTATTACCCATGGATACTATGATATATAAACTCTCGGAGGT
fle3lond5's/n.seq(1>5801) -> CGATTATAGAGCCAAGTTCGTTCCTCCATTTTGGCTTAATGCAATATTACAAGTAAATCTTATAAAACTTTCCATAAGTATCGTATTACCCATGGATACTATGATATATAAACTCTCGGAGGT

        1850      1860      1870      1880      1890      1900      1910      1920      1930      1940      1950      1960
        GTAGTCCAGAAGAAATGATCCATATTTGCATACAGTAAACTTGATGGAAAAAATATGTGGTACTGTTGGAATTGTAGCTATTGAGTATCAAATTTGAGAAAAAGGTAAAAAAATATGTAAAAT
fle3lond5's/n.seq(1>5801) -> GTAGTCCAGAAGAAATGATCCATATTTGCATACAGTAAACTTGATGGAAAAAATATGTGGTACTGTTGGAATTGTAGCTATTGAGTATCAAATTTGAGAAAAAGGTAAAAAAATATGTAAAAT

        1970      1980      1990      2000      2010      2020      2030      2040      2050      2060      2070      2080      2090
        TTGGGTGGAAGAAAAGAATTACATAAAATTGAGAATGTATGTAATTGACAAAATAATGTTTTCAAAACATAAAAACGTGATACCATTTAAATCCAAACCTTATATCATTTAACCATTTTTAG
fle3lond5's/n.seq(1>5801) -> TTGGGTGGAAGAAAAGAATTACATAAAATTGAGAATGTATGTAATTGACAAAATAATGTTTTCAAAACATAAAAACGTGATACCATTTAAATCCAAACCTTATATCATTTAACCATTTTTAG

        2100      2110      2120      2130      2140      2150      2160      2170      2180      2190      2200      2210
        TAAAACTAATAGTAATGAATGGTCAATAATATAAGATTACATATTAAATAATTACTACTTTCAGAAAATTTCAATCAAATCTATAATATTCCTTTGAAAAAAAAGAAAGACAAATAGGTAAAC
fle3lond5's/n.seq(1>5801) -> TAAAACTAATAGTAATGAATGGTCAATAATATAAGATTACATATTAAATAATTACTACTTTCAGAAAATTTCAATCAAATCTATAATATTCCTTTGAAAAAAAAGAAAGACAAATAGGTAAAC

        2220      2230      2240      2250      2260      2270      2280      2290      2300      2310      2320      2330
        TTCGATCGTATCAATCAAAGAATATATTTATTTTTCATCGTAACGTTTAATTCTAAGTCCTATTAAAAAACGTTAAATTTGATTTTTCTTACCATTTTTTTCTAAAAGGTGAGTTGTGTGTTG
fle3lond5's/n.seq(1>5801) -> TTCGATCGTATCAATCAAAGAATATATTTATTTTTCATCGTAACGTTTAATTCTAAGTCCTATTAAAAAACGTTAAATTTGATTTTTCTTACCATTTTTTTCTAAAAGGTGAGTTGTGTGTTG

        2340      2350      2360      2370      2380      2390      2400      2410      2420      2430      2440      2450      246
        TGTCAGGTCCAAAATAAAAGTTTGTCGTGAGGTCAAAATCTACGGTTACAGTAATTTTAATAACCTGTGAATCTGTGTCTAATCGAAAATTACAAAACACCAGTTGTTGTTGCATGAGAGACT
fle3lond5's/n.seq(1>5801) -> TGTCAGGTCCAAAATAAAAGTTTGTCGTGAGGTCAAAATCTACGGTTACAGTAATTTTAATAACCTGTGAATCTGTGTCTAATCGAAAATTACAAAACACCAGTTGTTGTTGCATGAGAGACT

        2470      2480      2490      2500      2510      2520      2530      2540      2550      2560      2570      2580
        TGTGAGCTTAGATTAGTGTGCGAGAGTCAGACAGAGAGAGAGATTTCGAATATCGAATGTCGAAGATAACCTTAGGGAACGAGTCAATAGTTGGGTCTTTGACTCCATCGAATAAGAAATCGT
fle3lond5's/n.seq(1>5801) -> TGTGAGCTTAGATTAGTGTGCGAGAGTCAGACAGAGAGAGAGATTTCGAATATCGAATGTCGAAGATAACCTTAGGGAACGAGTCAATAGTTGGGTCTTTGACTCCATCGAATAAGAAATCGT

        2590      2600      2610      2620      2630      2640      2650      2660      2670      2680      2690      2700
        ACAAAGTGACGAATAGGATTCAGGAAGGGAAGAAACCTTTGTATGCTGTTGTTTTCAACTTCCTTGATGCTCGTTTCTTCGATGTCTTCGTTACCGCTGGTGGAAATCGGGTAAAAGATCTCG
fle3lond5's/n.seq(1>5801) -> ACAAAGTGACGAATAGGATTCAGGAAGGGAAGAAACCTTTGTATGCTGTTGTTTTCAACTTCCTTGATGCTCGTTTCTTCGATGTCTTCGTTACCGCTGGTGGAAATCGGGTAAAAGATCTCG

        2710      2720      2730      2740      2750      2760      2770      2780      2790      2800      2810      2820
        ACTTTCAATTCGAAATCACTGTTTTCAATTCTGGGTCTGTTTAGGTTTTGATTCAGATTGATTGTAACATTAAGGCCTTTCCTTTTGTGTTTGATTTTGGATTCTGATTTCTAGCCTTTAGTG
fle3lond5's/n.seq(1>5801) -> ACTTTCAATTCGAAATCACTGTTTTCAATTCTGGGTCTGTTTAGGTTTTGATTCAGATTGATTGTAACATTAAGGCCTTTCCTTTTGTGTTTGATTTTGGATTCTGATTTCTAGCCTTTAGTG
cecln2(1>24)              ->                                                                 TGTAACATTAAGGCCTTTCCTTTT

        2830      2840      2850      2860      2870      2880      2890      2900      2910      2920      2930      2940      2950
        AGATTAAAAGATTGAAACTTTGCTTGATGCTATAGTCTAAGATTATGTAACATTTAGTTCAAACTTTCTGGTTTTGGAGATTTTGTGGAAGATATGGTTTTTGTTTTCTAATTTAAAGTGAAC
fle3lond5's/n.seq(1>5801) -> AGATTAAAAGATTGAAACTTTGCTTGATGCTATAGTCTAAGATTATGTAACATTTAGTTCAAACTTTCTGGTTTTGGAGATTTTGTGGAAGATATGGTTTTTGTTTTCTAATTTAAAGTGAAC
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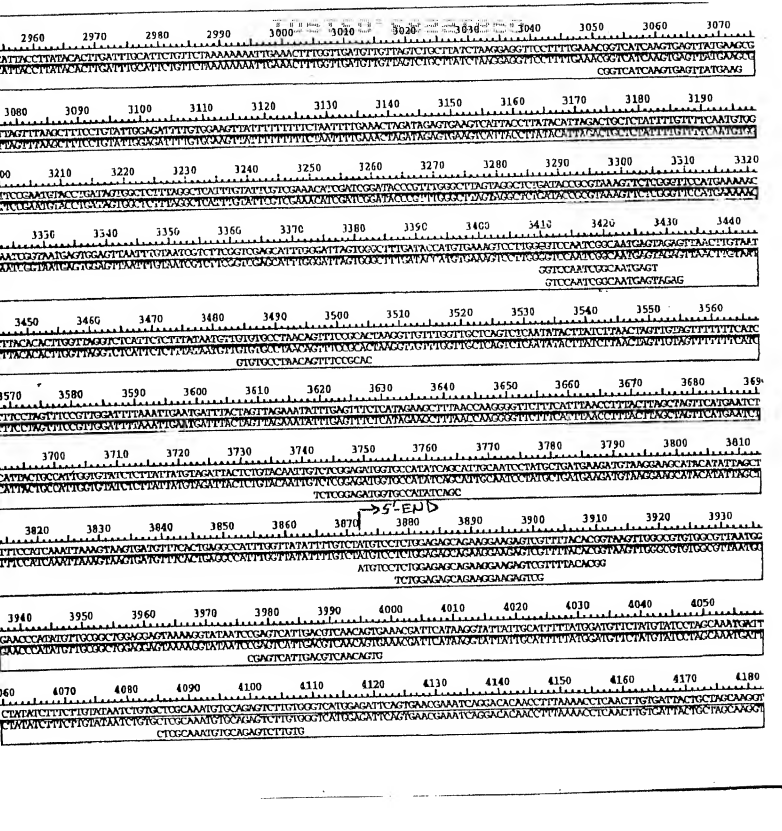
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CGGTCATCAAGTGAGTTATGAAG
3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190
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3200 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320
file1ond5's/n.seq(1>5801) ->
3330 3340 3350 3360 3370 3380 3390 3400 3410 3420 3430 3440
file1ond5's/n.seq(1>5801) ->
cer1s659(1>19) <-
cer1ns10596n(1>22) ->
GTCCAATCGGCAATGAGTAGAG
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Mir La-4Cla-S-S(1>22) <-
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3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800 3810
file1ond5's/n.seq(1>5801) ->
cer1ns10265n(1>24) ->
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3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930
5'END
file1ond5's/n.seq(1>5801) ->
file1cds5'.seq(1>40) ->
cer1ns10129n(1>24) ->
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TCTGGAGAGCAGAAGGAAGGAGTCG
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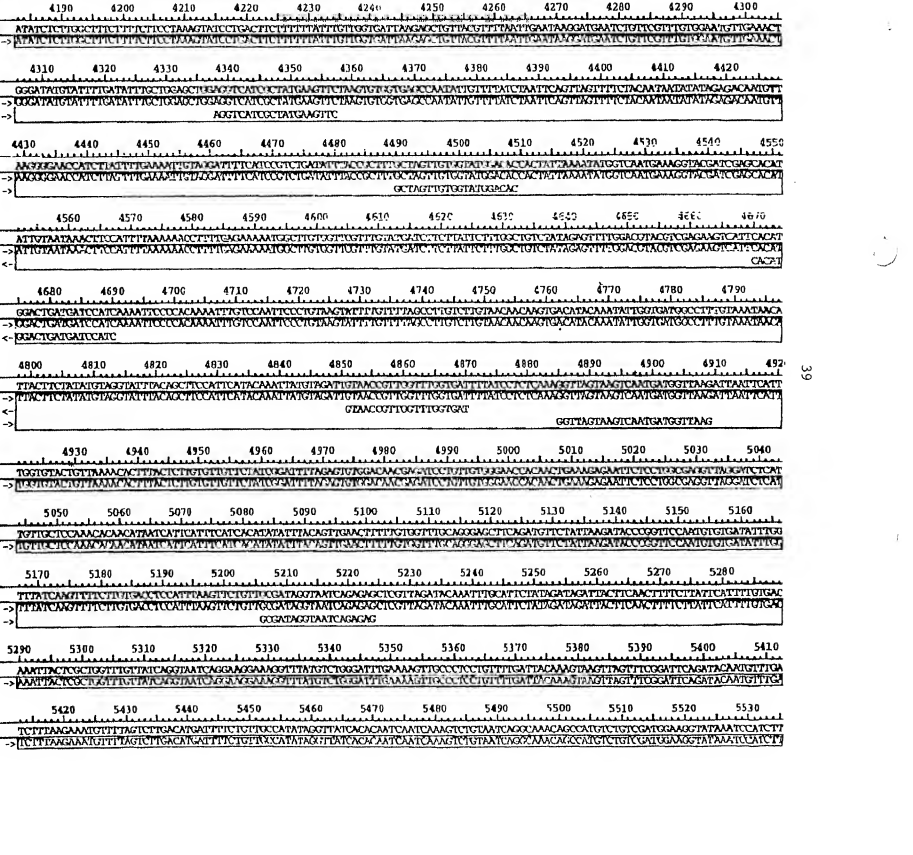
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cer1s2099(1>20)
Mir 8-4-N-N(1>25)
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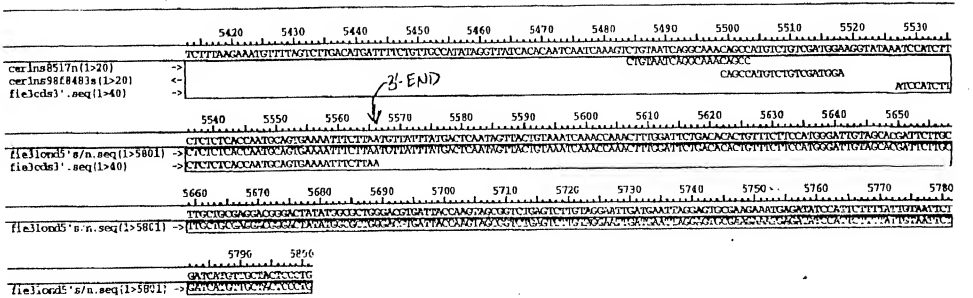
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cerlns8517n(1>20) ->
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file3lond5's/n.seq(1>5801) ->CTCTCTCACCAATGCAGTGAAAATTTCTTAATGTTATTTATGACTCAATAGTTACTGTAAATCAAACCAAACTTTGGATTCTGACACACTGTTTCTTCCATGGGATTGTAGCACGATTCTTGC
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file3lond5's/n.seq(1>5801) ->TTGCTGCGAGGACGGGACTATATCCCCTGGACGTGATTACCAAGTAGCGTCTGAGTCTTGTAGGAATTGATGAATTAGGAGTGCGAAGAAATGAGATATCCATCTTTTATTGTAAATTCT
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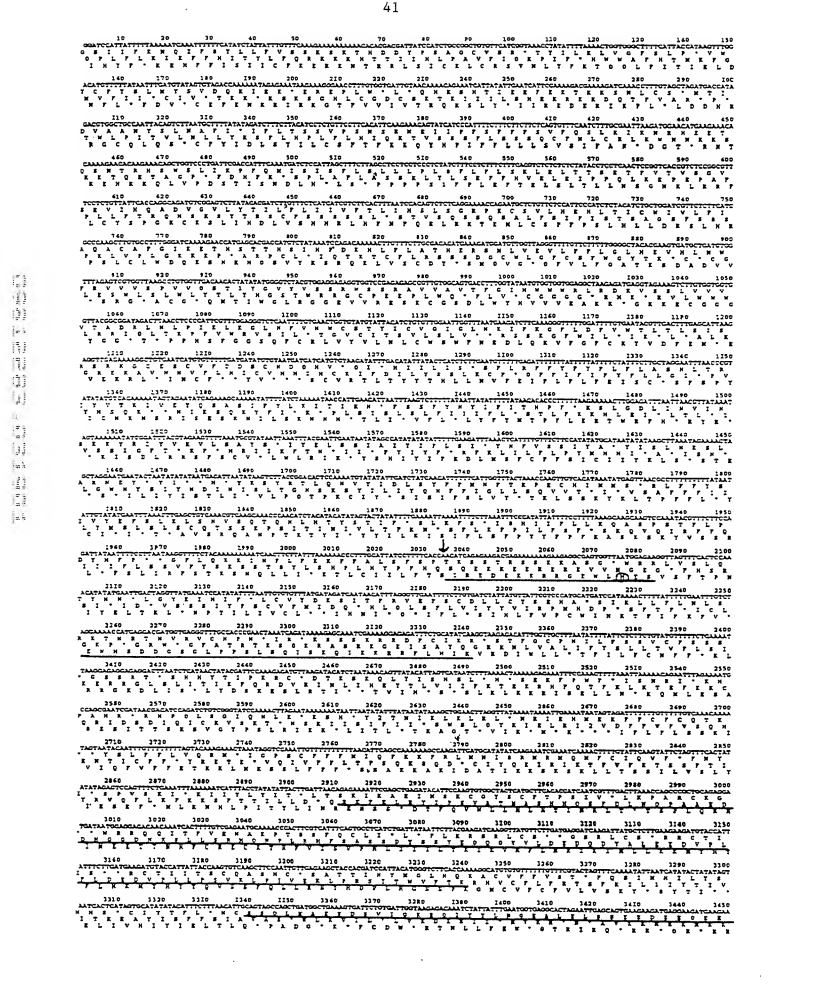

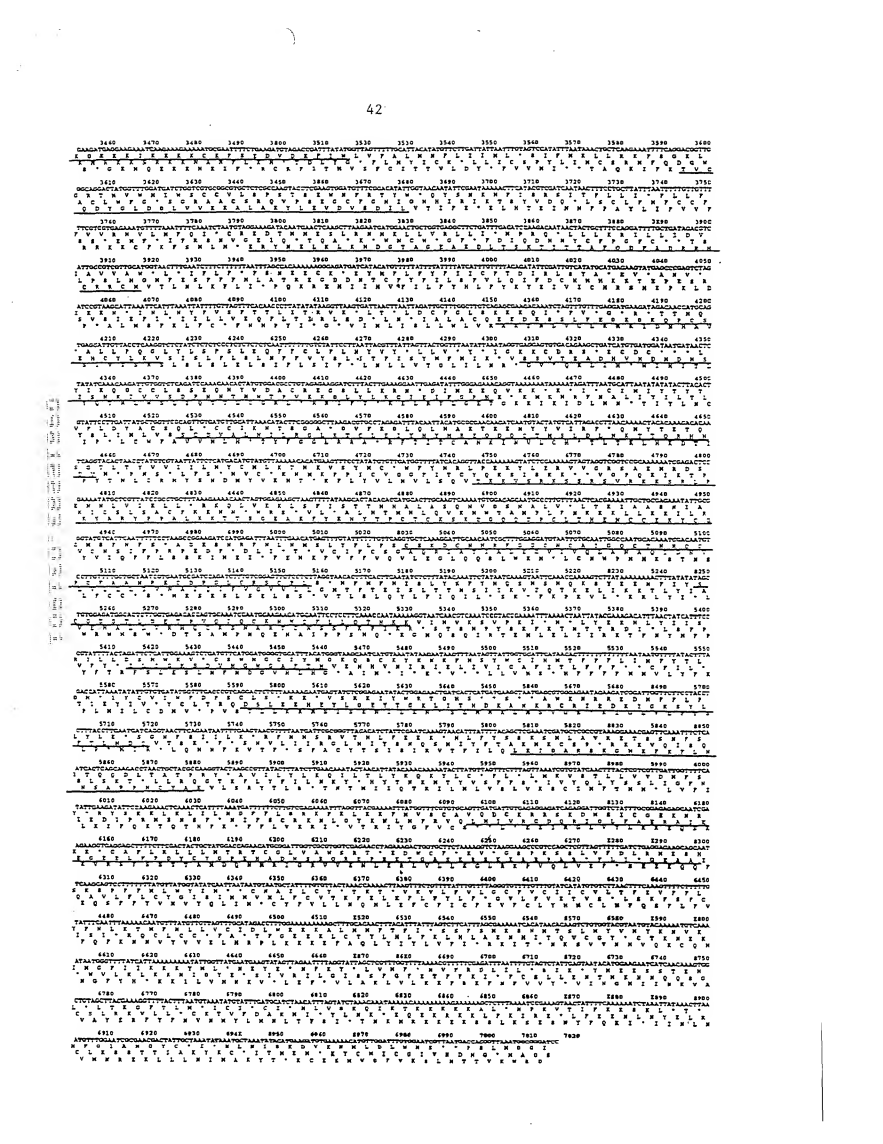

SEQUENCE LISTING

<110> Fischer, Robert L.
Ohad, Nir
Kiyosue, Tomohiro
Yadegari, Ramin
Margossian, Linda
Harada, John
Goldberg, Robert B.
The Regents of the University of California

<120> Nucleic Acids That Control Seed and Fruit Development in Plants

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<141> 1998-10-22

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Asn His Glu Asp Asp Gly Glu Gly Leu Pro Pro Glu Leu Asn Gln Ile
  5                  10                  15                  20

aaa gag caa atc gaa aag gag aga ttt ctg cat atc aag aga aaa ttc   150
Lys Glu Gln Ile Glu Lys Glu Arg Phe Leu His Ile Lys Arg Lys Phe
              25                  30                  35

gag ctg aga tac att cca agt gtg gct act cat gct tca cac cat caa   198
Glu Leu Arg Tyr Ile Pro Ser Val Ala Thr His Ala Ser His His Gln
          40                  45                  50

tcg ttt gac tta aac cag ccc gct gca gag gat gat aat gga gga gac   246
Ser Phe Asp Leu Asn Gln Pro Ala Ala Glu Asp Asp Asn Gly Gly Asp
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     70                  75                  80

gcc tca tct gat tat aat tct tac gaa gat caa ggt tat gtt ctt gat   342
Ala Ser Ser Asp Tyr Asn Ser Tyr Glu Asp Gln Gly Tyr Val Leu Asp
 85                  90                  95                 100

gag gat caa gat tat gct ctt gaa gaa gat gta cca tta ttt ctt gat   390
Glu Asp Gln Asp Tyr Ala Leu Glu Glu Asp Val Pro Leu Phe Leu Asp
                105                 110                 115

gaa gat gta cca tta tta cca agt gtc aag ctt cca att gtt gag aag   438
Glu Asp Val Pro Leu Leu Pro Ser Val Lys Leu Pro Ile Val Glu Lys
            120                 125                 130

cta cca cga tcc att aca tgg gtc ttc acc aaa agt agc cag ctg atg   486
Leu Pro Arg Ser Ile Thr Trp Val Phe Thr Lys Ser Ser Gln Leu Met
        135                 140                 145

gct gaa agt gat tct gtg att ggt aag aga caa atc tat tat ttg aat   534
Ala Glu Ser Asp Ser Val Ile Gly Lys Arg Gln Ile Tyr Tyr Leu Asn
    150                 155                 160

ggt gag gca cta gaa ttg agc agt gaa gaa gat gag gaa gat gaa gaa   582
Gly Glu Ala Leu Glu Leu Ser Ser Glu Glu Asp Glu Glu Asp Glu Glu
165                 170                 175                 180

gaa gat gag gaa gaa atc aag aaa gaa aaa tgc gaa ttt tct gaa gat   630
Glu Asp Glu Glu Glu Ile Lys Lys Glu Lys Cys Glu Phe Ser Glu Asp
                185                 190                 195

gta gac cga ttt ata tgg acg gtt ggg cag gac tat ggt ttg gat gat   678
Val Asp Arg Phe Ile Trp Thr Val Gly Gln Asp Tyr Gly Leu Asp Asp
            200                 205                 210

ctg gtc gtg cgg cgt gct ctc gcc aag tac ctc gaa gtg gat gtt tcg   726
Leu Val Val Arg Arg Ala Leu Ala Lys Tyr Leu Glu Val Asp Val Ser
        215                 220                 225

gac ata ttg gaa aga tac aat gaa ctc aag ctt aag aat gat gga act   774
Asp Ile Leu Glu Arg Tyr Asn Glu Leu Lys Leu Lys Asn Asp Gly Thr
    230                 235                 240

gct ggt gag gct tct gat ttg aca tcc aag aca ata act act gct ttc   822
Ala Gly Glu Ala Ser Asp Leu Thr Ser Lys Thr Ile Thr Thr Ala Phe
245                 250                 255                 260

cag gat ttt gct gat aga cgt cat tgc cgt cgt tgc atg ata ttc gat   870
Gln Asp Phe Ala Asp Arg Arg His Cys Arg Arg Cys Met Ile Phe Asp
                265                 270                 275

tgt cat atg cat gag aag tat gag ccc gag tct aga tcc agc gaa gac   918
Cys His Met His Glu Lys Tyr Glu Pro Glu Ser Arg Ser Ser Glu Asp
            280                 285                 290
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aaa tct agt ttg ttt gag gat gaa gat aga caa cca tgc agt gag cat   966
Lys Ser Ser Leu Phe Glu Asp Glu Asp Arg Gln Pro Cys Ser Glu His
        295                 300                 305

tgt tac ctc aag gtg agg agt gtg aca gaa gct gat cat gtg atg gat  1014
Cys Tyr Leu Lys Val Arg Ser Val Thr Glu Ala Asp His Val Met Asp
    310                 315                 320

aat gat aac tct ata tca aac aag att gtg gtc tca gat cca aac aac  1062
Asn Asp Asn Ser Ile Ser Asn Lys Ile Val Val Ser Asp Pro Asn Asn
325                 330                 335                 340

act atg tgg acg cct gta gag aag gat ctt tac ttg aaa gga att gag  1110
Thr Met Trp Thr Pro Val Glu Lys Asp Leu Tyr Leu Lys Gly Ile Glu
                345                 350                 355

ata ttt ggg aga aac agt tgt gat gtt gca tta aac ata ctt cgg ggg  1158
Ile Phe Gly Arg Asn Ser Cys Asp Val Ala Leu Asn Ile Leu Arg Gly
            360                 365                 370

ctt aag acg tgc cta gag att tac aat tac atg cgc gaa caa gat caa  1206
Leu Lys Thr Cys Leu Glu Ile Tyr Asn Tyr Met Arg Glu Gln Asp Gln
        375                 380                 385

tgt act atg tca tta gac ctt aac aaa act aca caa aga cac aat cag  1254
Cys Thr Met Ser Leu Asp Leu Asn Lys Thr Thr Gln Arg His Asn Gln
    390                 395                 400

gtt acc aaa aaa gta tct cga aaa agt agt agg tcg gtc cgc aaa aaa  1302
Val Thr Lys Lys Val Ser Arg Lys Ser Ser Arg Ser Val Arg Lys Lys
405                 410                 415                 420

tcg aga ctc cga aaa tat gct cgt tat ccg cct gct tta aag aaa aca  1350
Ser Arg Leu Arg Lys Tyr Ala Arg Tyr Pro Pro Ala Leu Lys Lys Thr
                425                 430                 435

act agt gga gaa gct aag ttt tat aag cac tac aca cca tgc act tgc  1398
Thr Ser Gly Glu Ala Lys Phe Tyr Lys His Tyr Thr Pro Cys Thr Cys
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aag tca aaa tgt gga cag caa tgc cct tgt tta act cac gaa aat tgc  1446
Lys Ser Lys Cys Gly Gln Gln Cys Pro Cys Leu Thr His Glu Asn Cys
        455                 460                 465

tgc gag aaa tat tgc ggg tgc tca aag gat tgc aac aat cgc ttt gga  1494
Cys Glu Lys Tyr Cys Gly Cys Ser Lys Asp Cys Asn Asn Arg Phe Gly
    470                 475                 480

gga tgt aat tgt gca att ggc caa tgc aca aat cga caa tgt cct tgt  1542
Gly Cys Asn Cys Ala Ile Gly Gln Cys Thr Asn Arg Gln Cys Pro Cys
485                 490                 495                 500

ttt gct gct aat cgt gaa tgc gat cca gat ctt tgt cgg agt tgt cct  1590
Phe Ala Ala Asn Arg Glu Cys Asp Pro Asp Leu Cys Arg Ser Cys Pro
                505                 510                 515
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ctt agc tgt gga gat ggc act ctt ggt gag aca cca gtg caa atc caa   1638
Leu Ser Cys Gly Asp Gly Thr Leu Gly Glu Thr Pro Val Gln Ile Gln
            520                 525                 530

tgc aag aac atg caa ttc ctc ctt caa acc aat aaa aag att ctc att   1686
Cys Lys Asn Met Gln Phe Leu Leu Gln Thr Asn Lys Lys Ile Leu Ile
        535                 540                 545

gga aag tct gat gtt cat gga tgg ggt gca ttt aca tgg gac tct ctt   1734
Gly Lys Ser Asp Val His Gly Trp Gly Ala Phe Thr Trp Asp Ser Leu
    550                 555                 560

aaa aag aat gag tat ctc gga gaa tat act gga gaa ctg atc act cat   1782
Lys Lys Asn Glu Tyr Leu Gly Glu Tyr Thr Gly Glu Leu Ile Thr His
565                 570                 575                 580

gat gaa gct aat gag cgt ggg aga ata gaa gat cgg att ggt tct tcc   1830
Asp Glu Ala Asn Glu Arg Gly Arg Ile Glu Asp Arg Ile Gly Ser Ser
                585                 590                 595

tac ctc ttt acc ttg aat gat cag ctc gaa atc gat gct cgc cgt aaa   1878
Tyr Leu Phe Thr Leu Asn Asp Gln Leu Glu Ile Asp Ala Arg Arg Lys
            600                 605                 610

gga aac gag ttc aaa ttt ctc aat cac tca gca aga cct aac tgc tac   1926
Gly Asn Glu Phe Lys Phe Leu Asn His Ser Ala Arg Pro Asn Cys Tyr
        615                 620                 625

gcc aag ttg atg att gtg aga gga gat cag agg att ggt cta ttt gcg   1974
Ala Lys Leu Met Ile Val Arg Gly Asp Gln Arg Ile Gly Leu Phe Ala
    630                 635                 640

gag aga gca atc gaa gaa ggt gag gag ctt ttc ttc gac tac tgc tat   2022
Glu Arg Ala Ile Glu Glu Gly Glu Glu Leu Phe Phe Asp Tyr Cys Tyr
645                 650                 655                 660

gga cca gaa cat gcg gat tgg tcg cgt ggt cga gaa cct aga aag act   2070
Gly Pro Glu His Ala Asp Trp Ser Arg Gly Arg Glu Pro Arg Lys Thr
                665                 670                 675

ggt gct tct aaa agg tct aag gaa gcc cgt cca gct cgt tagtttttga    2119
Gly Ala Ser Lys Arg Ser Lys Glu Ala Arg Pro Ala Arg
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            20                  25                  30

Lys Arg Lys Phe Glu Leu Arg Tyr Ile Pro Ser Val Ala Thr His Ala
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Ser His His Gln Ser Phe Asp Leu Asn Gln Pro Ala Ala Glu Asp Asp
    50                  55                  60

Asn Gly Gly Asp Asn Lys Ser Leu Leu Ser Arg Met Gln Asn Pro Leu
65                  70                  75                  80

Arg His Phe Ser Ala Ser Ser Asp Tyr Asn Ser Tyr Glu Asp Gln Gly
                85                  90                  95

Tyr Val Leu Asp Glu Asp Gln Asp Tyr Ala Leu Glu Glu Asp Val Pro
            100                 105                 110

Leu Phe Leu Asp Glu Asp Val Pro Leu Leu Pro Ser Val Lys Leu Pro
        115                 120                 125

Ile Val Glu Lys Leu Pro Arg Ser Ile Thr Trp Val Phe Thr Lys Ser
    130                 135                 140

Ser Gln Leu Met Ala Glu Ser Asp Ser Val Ile Gly Lys Arg Gln Ile
145                 150                 155                 160

Tyr Tyr Leu Asn Gly Glu Ala Leu Glu Leu Ser Ser Glu Glu Asp Glu
                165                 170                 175

Glu Asp Glu Glu Glu Asp Glu Glu Glu Ile Lys Lys Glu Lys Cys Glu
            180                 185                 190

Phe Ser Glu Asp Val Asp Arg Phe Ile Trp Thr Val Gly Gln Asp Tyr
        195                 200                 205

Gly Leu Asp Asp Leu Val Val Arg Arg Ala Leu Ala Lys Tyr Leu Glu
    210                 215                 220

Val Asp Val Ser Asp Ile Leu Glu Arg Tyr Asn Glu Leu Lys Leu Lys
225                 230                 235                 240

Asn Asp Gly Thr Ala Gly Glu Ala Ser Asp Leu Thr Ser Lys Thr Ile
                245                 250                 255

Thr Thr Ala Phe Gln Asp Phe Ala Asp Arg Arg His Cys Arg Arg Cys
            260                 265                 270

Met Ile Phe Asp Cys His Met His Glu Lys Tyr Glu Pro Glu Ser Arg
        275                 280                 285

Ser Ser Glu Asp Lys Ser Ser Leu Phe Glu Asp Glu Asp Arg Gln Pro
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Cys Ser Glu His Cys Tyr Leu Lys Val Arg Ser Val Thr Glu Ala Asp
305                 310                 315                 320
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His Val Met Asp Asn Asp Asn Ser Ile Ser Asn Lys Ile Val Val Ser
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Asp Pro Asn Asn Thr Met Trp Thr Pro Val Glu Lys Asp Leu Tyr Leu
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Lys Gly Ile Glu Ile Phe Gly Arg Asn Ser Cys Asp Val Ala Leu Asn
        355                 360                 365

Ile Leu Arg Gly Leu Lys Thr Cys Leu Glu Ile Tyr Asn Tyr Met Arg
    370                 375                 380

Glu Gln Asp Gln Cys Thr Met Ser Leu Asp Leu Asn Lys Thr Thr Gln
385                 390                 395                 400

Arg His Asn Gln Val Thr Lys Lys Val Ser Arg Lys Ser Ser Arg Ser
                405                 410                 415

Val Arg Lys Lys Ser Arg Leu Arg Lys Tyr Ala Arg Tyr Pro Pro Ala
            420                 425                 430

Leu Lys Lys Thr Thr Ser Gly Glu Ala Lys Phe Tyr Lys His Tyr Thr
        435                 440                 445

Pro Cys Thr Cys Lys Ser Lys Cys Gly Gln Gln Cys Pro Cys Leu Thr
    450                 455                 460

His Glu Asn Cys Cys Glu Lys Tyr Cys Gly Cys Ser Lys Asp Cys Asn
465                 470                 475                 480

Asn Arg Phe Gly Gly Cys Asn Cys Ala Ile Gly Gln Cys Thr Asn Arg
                485                 490                 495

Gln Cys Pro Cys Phe Ala Ala Asn Arg Glu Cys Asp Pro Asp Leu Cys
            500                 505                 510

Arg Ser Cys Pro Leu Ser Cys Gly Asp Gly Thr Leu Gly Glu Thr Pro
        515                 520                 525

Val Gln Ile Gln Cys Lys Asn Met Gln Phe Leu Leu Gln Thr Asn Lys
    530                 535                 540

Lys Ile Leu Ile Gly Lys Ser Asp Val His Gly Trp Gly Ala Phe Thr
545                 550                 555                 560

Trp Asp Ser Leu Lys Lys Asn Glu Tyr Leu Gly Glu Tyr Thr Gly Glu
                565                 570                 575

Leu Ile Thr His Asp Glu Ala Asn Glu Arg Gly Arg Ile Glu Asp Arg
            580                 585                 590

Ile Gly Ser Ser Tyr Leu Phe Thr Leu Asn Asp Gln Leu Glu Ile Asp
        595                 600                 605

Ala Arg Arg Lys Gly Asn Glu Phe Lys Phe Leu Asn His Ser Ala Arg
    610                 615                 620
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Pro Asn Cys Tyr Ala Lys Leu Met Ile Val Arg Gly Asp Gln Arg Ile
625                 630                 635                 640

Gly Leu Phe Ala Glu Arg Ala Ile Glu Glu Gly Glu Glu Leu Phe Phe
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agttgttgtt gcatgagaga cttgtgagct tagattagtg tgcgagagtc agacagagag 180

agagatttcg aatatcga atg tcg aag ata acc tta ggg aac gag tca ata   231
                    Met Ser Lys Ile Thr Leu Gly Asn Glu Ser Ile
                      1               5                  10

gtt ggg tct ttg act cca tcg aat aag aaa tcg tac aaa gtg acg aat   279
Val Gly Ser Leu Thr Pro Ser Asn Lys Lys Ser Tyr Lys Val Thr Asn
             15                  20                  25

agg att cag gaa ggg aag aaa cct ttg tat gct gtt gtt ttc aac ttc   327
Arg Ile Gln Glu Gly Lys Lys Pro Leu Tyr Ala Val Val Phe Asn Phe
         30                  35                  40

ctt gat gct cgt ttc ttc gat gtc ttc gtt acc gct ggt gga aat cgg   375
Leu Asp Ala Arg Phe Phe Asp Val Phe Val Thr Ala Gly Gly Asn Arg
     45                  50                  55

att act ctg tac aat tgt ctc gga gat ggt gcc ata tca gca ttg caa   423
Ile Thr Leu Tyr Asn Cys Leu Gly Asp Gly Ala Ile Ser Ala Leu Gln
 60                  65                  70                  75

tcc tat gct gat gaa gat aag gaa gag tcg ttt tac acg gta agt tgg   471
Ser Tyr Ala Asp Glu Asp Lys Glu Glu Ser Phe Tyr Thr Val Ser Trp
                 80                  85                  90
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ggt ata atc cga gtc att gac gtc aac agt gaa acg att cat aag agt   567
Gly Ile Ile Arg Val Ile Asp Val Asn Ser Glu Thr Ile His Lys Ser
        110                 115                 120

ctt gtg ggt cat gga gat tca gtg aac gaa atc agg aca caa cct tta   615
Leu Val Gly His Gly Asp Ser Val Asn Glu Ile Arg Thr Gln Pro Leu
    125                 130                 135

aaa cct caa ctt gtg att act gct agc aag gat gaa tct gtt cgt ttg   663
Lys Pro Gln Leu Val Ile Thr Ala Ser Lys Asp Glu Ser Val Arg Leu
140                 145                 150                 155

tgg aat gtt gaa act ggg ata tgt att ttg ata ttt gct gga gct gga   711
Trp Asn Val Glu Thr Gly Ile Cys Ile Leu Ile Phe Ala Gly Ala Gly
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ggt cat cgc tat gaa gtt cta agt gtg gat ttt cat ccg tct gat att   759
Gly His Arg Tyr Glu Val Leu Ser Val Asp Phe His Pro Ser Asp Ile
            175                 180                 185

tac cgc ttt gct agt tgt ggt atg gac acc act att aaa ata tgg tca   807
Tyr Arg Phe Ala Ser Cys Gly Met Asp Thr Thr Ile Lys Ile Trp Ser
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atg aaa gag ttt tgg acg tac gtc gag aag tca ttc aca tgg act gat   855
Met Lys Glu Phe Trp Thr Tyr Val Glu Lys Ser Phe Thr Trp Thr Asp
    205                 210                 215

gat cca tca aaa ttc ccc aca aaa ttt gtc caa ttc cct gta ttt aca   903
Asp Pro Ser Lys Phe Pro Thr Lys Phe Val Gln Phe Pro Val Phe Thr
220                 225                 230                 235

gct tcc att cat aca aat tat gta gat tgt aac cgt tgg ttt ggt gat   951
Ala Ser Ile His Thr Asn Tyr Val Asp Cys Asn Arg Trp Phe Gly Asp
                240                 245                 250

ttt atc ctc tca aag agt gtg gac aac gag atc ctg ttg tgg gaa cca   999
Phe Ile Leu Ser Lys Ser Val Asp Asn Glu Ile Leu Leu Trp Glu Pro
            255                 260                 265

caa ctg aaa gag aat tct cct ggc gag gga gct tca gat gtt cta tta   1047
Gln Leu Lys Glu Asn Ser Pro Gly Glu Gly Ala Ser Asp Val Leu Leu
        270                 275                 280

aga tac ccg gtt cca atg tgt gat att tgg ttt atc aag ttt tct tgt   1095
Arg Tyr Pro Val Pro Met Cys Asp Ile Trp Phe Ile Lys Phe Ser Cys
    285                 290                 295

gac ctc cat tta agt tct gtt gcg ata ggt aat cag gaa gga aag gtt   1143
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300                 305                 310                 315
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tat gtc tgg gat ttg aaa agt tgc cct cct gtt ttg att aca aag tta   1191
Tyr Val Trp Asp Leu Lys Ser Cys Pro Pro Val Leu Ile Thr Lys Leu
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tca cac aat caa tca aag tct gta atc agg caa aca gcc atg tct gtc   1239
Ser His Asn Gln Ser Lys Ser Val Ile Arg Gln Thr Ala Met Ser Val
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gat gga agc acg att ctt gct tgc tgc gag gac ggg act ata tgg cgc   1287
Asp Gly Ser Thr Ile Leu Ala Cys Cys Glu Asp Gly Thr Ile Trp Arg
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tgg gac gtg att acc aag tagcggtctg agtcttgtag gaattgatga          1335
Trp Asp Val Ile Thr Lys
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gtataccctt tctggagatt ttgtcttatt ctcttagttc aatacacaag gctgtatcct 1515

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Lys Lys Pro Leu Tyr Ala Val Val Phe Asn Phe Leu Asp Ala Arg Phe
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Phe Asp Val Phe Val Thr Ala Gly Gly Asn Arg Ile Thr Leu Tyr Asn
    50                  55                  60

Cys Leu Gly Asp Gly Ala Ile Ser Ala Leu Gln Ser Tyr Ala Asp Glu
65                  70                  75                  80

Asp Lys Glu Glu Ser Phe Tyr Thr Val Ser Trp Ala Cys Gly Val Asn
                85                  90                  95

Gly Asn Pro Tyr Val Ala Ala Gly Gly Val Lys Gly Ile Ile Arg Val
            100                 105                 110

Ile Asp Val Asn Ser Glu Thr Ile His Lys Ser Leu Val Gly His Gly
        115                 120                 125

Asp Ser Val Asn Glu Ile Arg Thr Gln Pro Leu Lys Pro Gln Leu Val
    130                 135                 140
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Ile Thr Ala Ser Lys Asp Glu Ser Val Arg Leu Trp Asn Val Glu Thr
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Gly Ile Cys Ile Leu Ile Phe Ala Gly Ala Gly Gly His Arg Tyr Glu
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Val Leu Ser Val Asp Phe His Pro Ser Asp Ile Tyr Arg Phe Ala Ser
            180                 185                 190

Cys Gly Met Asp Thr Thr Ile Lys Ile Trp Ser Met Lys Glu Phe Trp
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Thr Tyr Val Glu Lys Ser Phe Thr Trp Thr Asp Asp Pro Ser Lys Phe
    210                 215                 220

Pro Thr Lys Phe Val Gln Phe Pro Val Phe Thr Ala Ser Ile His Thr
225                 230                 235                 240

Asn Tyr Val Asp Cys Asn Arg Trp Phe Gly Asp Phe Ile Leu Ser Lys
                245                 250                 255

Ser Val Asp Asn Glu Ile Leu Leu Trp Glu Pro Gln Leu Lys Glu Asn
            260                 265                 270

Ser Pro Gly Glu Gly Ala Ser Asp Val Leu Leu Arg Tyr Pro Val Pro
        275                 280                 285

Met Cys Asp Ile Trp Phe Ile Lys Phe Ser Cys Asp Leu His Leu Ser
    290                 295                 300

Ser Val Ala Ile Gly Asn Gln Glu Gly Lys Val Tyr Val Trp Asp Leu
305                 310                 315                 320

Lys Ser Cys Pro Pro Val Leu Ile Thr Lys Leu Ser His Asn Gln Ser
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Lys Ser Val Ile Arg Gln Thr Ala Met Ser Val Asp Gly Ser Thr Ile
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Leu Ala Cys Cys Glu Asp Gly Thr Ile Trp Arg Trp Asp Val Ile Thr
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Lys
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WD40/polycomb gene genomic sequence

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SET/polycomb gene genomic sequence reading frame 1

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SET/polycomb gene genomic sequence reading frame 2

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1 5 10 15

tca aag aaa aaa aaa aca cac gac gat tat cca tct gcc ggc tgt gtt 96
Ser Lys Lys Lys Lys Thr His Asp Asp Tyr Pro Ser Ala Gly Cys Val
20 25 30

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cat cgg taa acc tat att tta aaa ctg gtg ggc ttt tca tta cca taa   144
His Arg     Thr Tyr Ile Leu Lys Leu Val Gly Phe Ser Leu Pro
         35                  40                  45

gtt tgg aca tgt ttt tat aat ttg atg tat agt gta gac caa aaa ata   192
Val Trp Thr Cys Phe Tyr Asn Leu Met Tyr Ser Val Asp Gln Lys Ile
     50                  55                  60

gag aaa taa gaa agg gaa cct ttg tgg tga ttg taa caa aac aga aat   240
Glu Lys     Glu Arg Glu Pro Leu Trp     Leu     Gln Asn Arg Asn
 65                  70                  75                  80

cat tat att gaa tca ttc gaa aag acg aaa aga tca aac ctt tgt agc   288
His Tyr Ile Glu Ser Phe Glu Lys Thr Lys Arg Ser Asn Leu Cys Ser
                 85                  90                  95

tag atg acc ata gac gtg gct gcc aat tac agt ctt aat gct ttt ata   336
    Met Thr Ile Asp Val Ala Ala Asn Tyr Ser Leu Asn Ala Phe Ile
            100                 105                 110

tag atc ttt ctt aca tcc tct gtt cct tca cat tca aga aac agt atc   384
    Ile Phe Leu Thr Ser Ser Val Pro Ser His Ser Arg Asn Ser Ile
        115                 120                 125

atc cca ttt tct ttc ttc ttc tca gtg ttt caa tct ttg cga att aag   432
Ile Pro Phe Ser Phe Phe Phe Ser Val Phe Gln Ser Leu Arg Ile Lys
    130                 135                 140

atg gaa cat gaa gaa aca caa aag aac aca aga aac agc tgg tcc ctg   480
Met Glu His Glu Glu Thr Gln Lys Asn Thr Arg Asn Ser Trp Ser Leu
145                 150                 155                 160

att cga cca ttt caa atg atc tcc att agc ttt ctt agc ctc ctc ctc   528
Ile Arg Pro Phe Gln Met Ile Ser Ile Ser Phe Leu Ser Leu Leu Leu
                165                 170                 175

cct cta tct ttc ctc ttt ctt tca cgt ctc tct ctc tat acc tcc tca   576
Pro Leu Ser Phe Leu Phe Leu Ser Arg Leu Ser Leu Tyr Thr Ser Ser
            180                 185                 190

act ccg gtc acc gtc tcc ggc gtt tcc tct gtt att cac cag gca gat   624
Thr Pro Val Thr Val Ser Gly Val Ser Ser Val Ile His Gln Ala Asp
        195                 200                 205

gtc gga gtc tta tac acg atc ttg ttt ctc atc atc gtc ttc act tta   672
Val Gly Val Leu Tyr Thr Ile Leu Phe Leu Ile Ile Val Phe Thr Leu
    210                 215                 220

atc cac agt ctc tca gga aaa cca gaa tgc tct gtt ctc cat tcc cat   720
Ile His Ser Leu Ser Gly Lys Pro Glu Cys Ser Val Leu His Ser His
225                 230                 235                 240

ctc tac atc tgc tgg atc gtt ctc ttc atc gcc caa gct tgt gcc ttt   768
Leu Tyr Ile Cys Trp Ile Val Leu Phe Ile Ala Gln Ala Cys Ala Phe
                245                 250                 255
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ggg atc aaa aga acc atg agc acg acc atg tct ata aat cca gac aaa   816
Gly Ile Lys Arg Thr Met Ser Thr Thr Met Ser Ile Asn Pro Asp Lys
            260                 265                 270

aac ttg ttt ctt gcg aca cat gaa aga tgg atg ttg gtt agg gtt ttg   864
Asn Leu Phe Leu Ala Thr His Glu Arg Trp Met Leu Val Arg Val Leu
        275                 280                 285

ttc ttt ttg ggg cta cac gaa gtg atg ctg atg tgg ttt aga gtc gtg   912
Phe Phe Leu Gly Leu His Glu Val Met Leu Met Trp Phe Arg Val Val
    290                 295                 300

gtt aag cct gtg gtt gac aac act ata tat ggg gtc tac gtg gag gag   960
Val Lys Pro Val Val Asp Asn Thr Ile Tyr Gly Val Tyr Val Glu Glu
305                 310                 315                 320

agg tgg tcc gag aga gcc gtt gtg gca gtg acc ttt ggt ata atg tgg  1008
Arg Trp Ser Glu Arg Ala Val Val Ala Val Thr Phe Gly Ile Met Trp
                325                 330                 335

tgg tgg agg cta aga gat gag gta gaa agt ctt gtg gtg gtg gtt acg  1056
Trp Trp Arg Leu Arg Asp Glu Val Glu Ser Leu Val Val Val Val Thr
            340                 345                 350

gcg gat aga ctt aac ctc ccc att cgt ttg gag ggt ctc aat ttt gtg  1104
Ala Asp Arg Leu Asn Leu Pro Ile Arg Leu Glu Gly Leu Asn Phe Val
        355                 360                 365

aac tgg tgt atg tat tac atc tgt gtt gga att ggt tta atg aag atc  1152
Asn Trp Cys Met Tyr Tyr Ile Cys Val Gly Ile Gly Leu Met Lys Ile
    370                 375                 380

ttc aaa ggg ttt ttg gat ttt gtg aat acg ttg act ttg agc att aag  1200
Phe Lys Gly Phe Leu Asp Phe Val Asn Thr Leu Thr Leu Ser Ile Lys
385                 390                 395                 400

agg tcg aga aaa ggc tgt gaa tca tgt gtt ttt gat gat atg tgt aat  1248
Arg Ser Arg Lys Gly Cys Glu Ser Cys Val Phe Asp Asp Met Cys Asn
                405                 410                 415

gat gat cat gtg taa gat att tga cat att ata ctc atc tct tga atg  1296
Asp Asp His Val     Asp Ile     His Ile Ile Leu Ile Ser     Met
            420                 425                 430

ttt ttg aga ttt ttt tat ttt tat ttt cta ttt ctt gct agg aat tta  1344
Phe Leu Arg Phe Phe Tyr Phe Tyr Phe Leu Phe Leu Ala Arg Asn Leu
        435                 440                 445

acc cgt ata tat gtc aca aaa ata gta gaa tat cag aaa gca aaa ata  1392
Thr Arg Ile Tyr Val Thr Lys Ile Val Glu Tyr Gln Lys Ala Lys Ile
    450                 455                 460

ttt tat cta aaa ata acc att gaa cat taa ttt aag tct ttt tat aat  1440
Phe Tyr Leu Lys Ile Thr Ile Glu His     Phe Lys Ser Phe Tyr Asn
465                 470                 475                 480
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tat att ttt ata aca cac cct ttt taa gaa aaa ctt gga gat tta att   1488
Tyr Ile Phe Ile Thr His Pro Phe     Glu Lys Leu Gly Asp Leu Ile
                485                 490                 495

aac gtt ata aat agt aaa aaa tat cgg att tac gta gaa gtt tta aat   1536
Asn Val Ile Asn Ser Lys Lys Tyr Arg Ile Tyr Val Glu Val Leu Asn
            500                 505                 510

gcg tat aat taa att tac gaa ttg aat aat ata gcc ata tat ata ttt   1584
Ala Tyr Asn     Ile Tyr Glu Leu Asn Asn Ile Ala Ile Tyr Ile Phe
        515                 520                 525

ttg aag att taa act cat ttt gtt tct tcc ata tat gca taa tat ata   1632
Leu Lys Ile     Thr His Phe Val Ser Ser Ile Tyr Ala     Tyr Ile
    530                 535                 540

agc tta aat aga aaa cta gct agg aat gaa tac taa tat ata taa tga   1680
Ser Leu Asn Arg Lys Leu Ala Arg Asn Glu Tyr     Tyr Ile
545                 550                 555                 560

cat taa tat aag tct tac cgg aca ctc caa aat gta tat att gat cta   1728
His     Tyr Lys Ser Tyr Arg Thr Leu Gln Asn Val Tyr Ile Asp Leu
                565                 570                 575

tca aca ttt ttt cat tgg ttt act aaa cca agt tgt cac ata aat atg   1776
Ser Thr Phe Phe His Trp Phe Thr Lys Pro Ser Cys His Ile Asn Met
            580                 585                 590

agt taa cgc ctt ttt ttt tat aat att gta tat gaa ttt aaa ctt gag   1824
Ser     Arg Leu Phe Phe Tyr Asn Ile Val Tyr Glu Phe Lys Leu Glu
        595                 600                 605

ctg tca aac gtc aag caa acc caa cat cta cat aca tat agt act ata   1872
Leu Ser Asn Val Lys Gln Thr Gln His Leu His Thr Tyr Ser Thr Ile
    610                 615                 620

ttt tga aaa tta aaa ttt tct taa att tcc cat att att ttc ctt tta   1920
Phe     Lys Leu Lys Phe Ser     Ile Ser His Ile Ile Phe Leu Leu
625                 630                 635                 640

aag caa gca agt cca aat acg ttt ctt cca gat tat aat ttt cct taa   1968
Lys Gln Ala Ser Pro Asn Thr Phe Leu Pro Asp Tyr Asn Phe Pro
                645                 650                 655

taa ggt ttt cta caa aaa aaa atc aac ttc tta ttt aaa aaa ccc ttt   2016
    Gly Phe Leu Gln Lys Lys Ile Asn Phe Leu Phe Lys Lys Pro Phe
            660                 665                 670

gca tta tcc ttt tca cca aca tca gag aag acg aga aaa aaa gaa gag   2064
Ala Leu Ser Phe Ser Pro Thr Ser Glu Lys Thr Arg Lys Lys Glu Glu
        675                 680                 685

gcg agt ggt taa tgg aga agg tta gtt tca ctc caa aca tat atg aat   2112
Ala Ser Gly     Trp Arg Arg Leu Val Ser Leu Gln Thr Tyr Met Asn
    690                 695                 700
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tga cta ggt tat gaa atc cat ata ttt taa ttg tgt gtt tat gat aga   2160
    Leu Gly Tyr Glu Ile His Ile Phe     Leu Cys Val Tyr Asp Arg
705                 710                 715                 720

tca ata aca ttt agg gtt gaa ttt tct tgt gat cta tta tgt tat tcg   2208
Ser Ile Thr Phe Arg Val Glu Phe Ser Cys Asp Leu Leu Cys Tyr Ser
                725                 730                 735

tcc cat gca tga tcc ata aaa ctt tta ttt ttg aat ttg tct agg aaa   2256
Ser His Ala     Ser Ile Lys Leu Leu Phe Leu Asn Leu Ser Arg Lys
            740                 745                 750

acc atg agg acg atg gtg agg gtt tgc cac ccg aac taa atc aga taa   2304
Thr Met Arg Thr Met Val Arg Val Cys His Pro Asn     Ile Arg
        755                 760                 765

aag agc aaa tcg aaa agg aga gat ttc tgc ata tca agg taa gag aca   2352
Lys Ser Lys Ser Lys Arg Arg Asp Phe Cys Ile Ser Arg     Glu Thr
    770                 775                 780

ttt ggt tgc ttt aat att tta ttc tct tct gta tgt ttt tct gaa aat   2400
Phe Gly Cys Phe Asn Ile Leu Phe Ser Ser Val Cys Phe Ser Glu Asn
785                 790                 795                 800

taa gga gag gag agg act taa tct cat aac tat acg att cca aag aga   2448
    Gly Glu Glu Arg Thr     Ser His Asn Tyr Thr Ile Pro Lys Arg
                805                 810                 815

tgt taa gat aca tct aat aaa cag tta tac att agt cat aat ctt taa   2496
Cys     Asp Thr Ser Asn Lys Gln Leu Tyr Ile Ser His Asn Leu
            820                 825                 830

aac taa aaa gag aaa ttt cca aac ttt taa att aaa aac aga att tag   2544
Asn     Lys Glu Lys Phe Pro Asn Phe     Ile Lys Asn Arg Ile
        835                 840                 845

aaa atg cca gcg aat cga taa cga cat cca gat ctg tcg ggt atc caa   2592
Lys Met Pro Ala Asn Arg     Arg His Pro Asp Leu Ser Gly Ile Gln
    850                 855                 860

aac tta gaa taa aaa aat aat taa tat att tat aat ata aag ctg gaa   2640
Asn Leu Glu     Lys Asn Asn     Tyr Ile Tyr Asn Ile Lys Leu Glu
865                 870                 875                 880

ctt agg tta taa aat aaa att gaa aat aat agt aga ttt ttt tgt ttt   2688
Leu Arg Leu     Asn Lys Ile Glu Asn Asn Ser Arg Phe Phe Cys Phe
                885                 890                 895

tgt caa aca aaa tag taa tac aat ttg ttt ttt tta gta caa aga aac   2736
Cys Gln Thr Lys         Tyr Asn Leu Phe Phe Leu Val Gln Arg Asn
            900                 905                 910

taa ata ggt cca aat tgt ttt ttt ttt aac att cag cca aaa aag cca   2784
    Ile Gly Pro Asn Cys Phe Phe Phe Asn Ile Gln Pro Lys Lys Pro
        915                 920                 925
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aga ttg atg cat ata tca aga aat cga aat caa aac ttt tgt att caa   2832
Arg Leu Met His Ile Ser Arg Asn Arg Asn Gln Asn Phe Cys Ile Gln
    930                 935                 940

gta ttc tag ttt cac tat ata tag agt cca gtt tct gaa att taa aaa   2880
Val Phe     Phe His Tyr Ile     Ser Pro Val Ser Glu Ile     Lys
945                 950                 955                 960

atc att tac cta tat att act tga tta aca gag aaa att cga gct gag   2928
Ile Ile Tyr Leu Tyr Ile Thr     Leu Thr Glu Lys Ile Arg Ala Glu
                965                 970                 975

ata cat tcc aag tgt ggc tac tca tgc ttc aca cca tca atc gtt tga   2976
Ile His Ser Lys Cys Gly Tyr Ser Cys Phe Thr Pro Ser Ile Val
            980                 985                 990

ctt aaa cca gcc cgc tgc aga gga tga taa tgg agg aga caa caa atc   3024
Leu Lys Pro Ala Arg Cys Arg Gly         Trp Arg Arg Gln Gln Ile
        995                1000                1005

act ttt gtc gag aat gca aaa ccc act tcg tca ttt cag tgc ctc atc   3072
Thr Phe Val Glu Asn Ala Lys Pro Thr Ser Ser Phe Gln Cys Leu Ile
    1010                1015                1020

tga tta taa ttc tta cga aga tca agg tta tgt tct tga tga gga tca   3120
    Leu     Phe Leu Arg Arg Ser Arg Leu Cys Ser         Gly Ser
1025                1030                1035                1040

aga tta tgc tct tga aga aga tgt acc att att tct tga tga aga tgt   3168
Arg Leu Cys Ser     Arg Arg Cys Thr Ile Ile Ser         Arg Cys
                1045                1050                1055

acc att att acc aag tgt caa gct tcc aat tgt tga gaa gct acc acg   3216
Thr Ile Ile Thr Lys Cys Gln Ala Ser Asn Cys     Glu Ala Thr Thr
            1060                1065                1070

atc cat tac atg ggt ctt cac caa aag gca tgt gtg ttt ttt gtt tcg   3264
Ile His Tyr Met Gly Leu His Gln Lys Ala Cys Val Phe Phe Val Ser
        1075                1080                1085

tac tag ttt caa aat att aat cat ata cta tat agt aat cac tca tag   3312
Tyr     Phe Gln Asn Ile Asn His Ile Leu Tyr Ser Asn His Ser
    1090                1095                1100

tgc ata tat aca ttt ctt taa cat tgc agt agc cag ctg atg gct gaa   3360
Cys Ile Tyr Thr Phe Leu     His Cys Ser Ser Gln Leu Met Ala Glu
1105                1110                1115                1120

agt gat tct gtg att ggt aag aga caa atc tat tat ttg aat ggt gag   3408
Ser Asp Ser Val Ile Gly Lys Arg Gln Ile Tyr Tyr Leu Asn Gly Glu
                1125                1130                1135

gca cta gaa ttg agc agt gaa gaa gat gag gaa gat gaa gaa gaa gat   3456
Ala Leu Glu Leu Ser Ser Glu Glu Asp Glu Glu Asp Glu Glu Glu Asp
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gag gaa gaa atc aag aaa gaa aaa tgc gaa ttt tct gaa gat gta gac   3504
Glu Glu Glu Ile Lys Lys Glu Lys Cys Glu Phe Ser Glu Asp Val Asp
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cga ttt ata tgg tta gtt ttt gca tta cat atg ttc ttg att att aat   3552
Arg Phe Ile Trp Leu Val Phe Ala Leu His Met Phe Leu Ile Ile Asn
    1170                1175                1180

ttg tag tcc ata ttt aat aaa ctg ctc aag aaa ttt tca gga cgg ttg   3600
Leu     Ser Ile Phe Asn Lys Leu Leu Lys Lys Phe Ser Gly Arg Leu
1185                1190                1195                1200

ggc agg act atg gtt tgg atg atc tgg tcg tgc ggc gtg ctc tcg cca   3648
Gly Arg Thr Met Val Trp Met Ile Trp Ser Cys Gly Val Leu Ser Pro
                1205                1210                1215

agt acc tcg aag tgg atg ttt cgg aca tat tgg taa caa tat tcg aat   3696
Ser Thr Ser Lys Trp Met Phe Arg Thr Tyr Trp     Gln Tyr Ser Asn
            1220                1225                1230

aaa aac ttc ata cgt cga tca ata act ttc ctg ctt att taa ttt ttg   3744
Lys Asn Phe Ile Arg Arg Ser Ile Thr Phe Leu Leu Ile     Phe Leu
        1235                1240                1245

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Leu Phe Phe Val Val Arg Asn Val Leu Asn Phe Gln Ile     Cys Arg
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aaa gat aca atg aac tca agc tta aga atg atg gaa ctg ctg gtg agg   3840
Lys Asp Thr Met Asn Ser Ser Leu Arg Met Met Glu Leu Leu Val Arg
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ctt ctg att tga cat cca aga caa taa cta ctg ctt tcc agg att ttg   3888
Leu Leu Ile     His Pro Arg Gln     Leu Leu Leu Ser Arg Ile Leu
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ctg ata gac gtc att gcc gtc gtt gca tgg taa ctt tga atc ttt ctt   3936
Leu Ile Asp Val Ile Ala Val Val Ala Trp     Leu     Ile Phe Leu
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Phe     Phe Ser His Lys Lys Gly Arg     Ser Tyr Met Phe Leu Phe
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tat ttt atc att tgt ttt aca gat att cga ttg tca tat gca tga gaa   4032
Tyr Phe Ile Ile Cys Phe Thr Asp Ile Arg Leu Ser Tyr Ala     Glu
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gta tga gcc cga gtc tag atc cgt aag cat taa att cat tta aat tat   4080
Val     Ala Arg Val     Ile Arg Lys His     Ile His Leu Asn Tyr
1345                1350                1355                1360

ttt gtt agt ttc aca acc ctt ata tat aag gtt aag tga tta act taa   4128
Phe Val Ser Phe Thr Thr Leu Ile Tyr Lys Val Lys     Leu Thr
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tta gat tgc ttt ggc ttg tca gag cga aga caa atc tag ttt gtt tga   4176
Leu Asp Cys Phe Gly Leu Ser Glu Arg Arg Gln Ile     Phe Val
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gga tga aga tag aca acc atg cag tga gca ttg tta cct caa ggt ctc   4224
Gly     Arg     Thr Thr Met Gln     Ala Leu Leu Pro Gln Gly Leu
      1395                1400                1405

tat ctc tct ccc tct ctc tct caa ttt ttt tgt cta ttc ctt aat tac   4272
Tyr Leu Ser Pro Ser Leu Ser Gln Phe Phe Cys Leu Phe Leu Asn Tyr
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gtt tat tag tta ctg gtt taa tat taa ata ggt gag gag tgt gac aga   4320
Val Tyr     Leu Leu Val     Tyr     Ile Gly Glu Glu Cys Asp Arg
1425                1430                1435                1440

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Ser     Ser Cys Asp Gly             Leu Tyr Ile Lys Gln Asp Cys
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ggt ctc aga tcc aaa caa cac tat gtg gac gcc tgt aga gaa gga tct   4416
Gly Leu Arg Ser Lys Gln His Tyr Val Asp Ala Cys Arg Glu Gly Ser
          1460                1465                1470

tta ctt gaa agg aat tga gat att tgg gag aaa cag gta aaa aaa taa   4464
Leu Leu Glu Arg Asn     Asp Ile Trp Glu Lys Gln Val Lys Lys
      1475                1480                1485

aaa tag att taa tgc att aat ata tat act tac act gta ttc ctt gat   4512
Lys     Ile     Cys Ile Asn Ile Tyr Thr Tyr Thr Val Phe Leu Asp
   1490                1495                1500

tat gct ggt tcg cag ttg tga tgt tgc att aaa cat act tcg ggg gct   4560
Tyr Ala Gly Ser Gln Leu     Cys Cys Ile Lys His Thr Ser Gly Ala
1505                1510                1515                1520

taa gac gtg cct aga gat tta caa tta cat gcg cga aca aga tca atg   4608
    Asp Val Pro Arg Asp Leu Gln Leu His Ala Arg Thr Arg Ser Met
              1525                1530                1535

tac tat gtc att aga cct taa caa aac tac aca aag aca caa tca ggt   4656
Tyr Tyr Val Ile Arg Pro     Gln Asn Tyr Thr Lys Thr Gln Ser Gly
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aca cta acc tat gtc gta att att ctc atg aca tgt atg tta aaa aca   4704
Thr Leu Thr Tyr Val Val Ile Ile Leu Met Thr Cys Met Leu Lys Thr
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cat gaa gtt tcc tat atg tgt tga tgg ttt tat cac agg tta cca aaa   4752
His Glu Val Ser Tyr Met Cys     Trp Phe Tyr His Arg Leu Pro Lys
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aag tat ctc gaa aaa gta gta ggt cgg tcc gca aaa aat cga gac tcc   4800
Lys Tyr Leu Glu Lys Val Val Gly Arg Ser Ala Lys Asn Arg Asp Ser
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gaa aat atg ctc gtt atc cgc ctg ctt taa aga aaa caa cta gtg gag   4848
Glu Asn Met Leu Val Ile Arg Leu Leu     Arg Lys Gln Leu Val Glu
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aag cta agt ttt ata agc act aca cac cat gca ctt gca agt caa aat   4896
Lys Leu Ser Phe Ile Ser Thr Thr His His Ala Leu Ala Ser Gln Asn
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gtg gac agc aat gcc ctt gtt taa ctc acg aaa att gct gcg aga aat   4944
Val Asp Ser Asn Ala Leu Val     Leu Thr Lys Ile Ala Ala Arg Asn
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att gcg ggt atg tca ttc aat ttt tcc taa gcc gga aga tcc atg aga   4992
Ile Ala Gly Met Ser Phe Asn Phe Ser     Ala Gly Arg Ser Met Arg
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Phe Asn Leu Asn Met Ser Leu Tyr Phe Leu Phe Arg Cys Ser Lys Asp
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Cys Asn Asn Arg Phe Gly Gly Cys Asn Cys Ala Ile Gly Gln Cys Thr
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Asn Arg Gln Cys Pro Cys Phe Ala Ala Asn Arg Glu Cys Asp Pro Asp
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Leu Cys Arg Ser Cys Pro Leu Arg     His Phe His Phe Asn Ile Ser
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tta tac aaa ttc tat aat caa agt aat tca aac caa aag tct tat aaa   5232
Leu Tyr Lys Phe Tyr Asn Gln Ser Asn Ser Asn Gln Lys Ser Tyr Lys
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aaa aac ttt ata tat agc tgt gga gat ggc act ctt ggt gag aca cca   5280
Lys Asn Phe Ile Tyr Ser Cys Gly Asp Gly Thr Leu Gly Glu Thr Pro
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gtg caa atc caa tgc aag aac atg caa ttc ctc ctt caa acc aat aaa   5328
Val Gln Ile Gln Cys Lys Asn Met Gln Phe Leu Leu Gln Thr Asn Lys
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aag gta atc aac gtc aaa tcc gta ccg aaa att taa aac taa tta tac   5376
Lys Val Ile Asn Val Lys Ser Val Pro Lys Ile     Asn     Leu Tyr
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gaa aga cat tta act atc att tcc cgt att tta cta gat tct cat tgg   5424
Glu Arg His Leu Thr Ile Ile Ser Arg Ile Leu Leu Asp Ser His Trp
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aaa gtc tga tgt tca tgg atg ggg tgc att tac atg ggt aag caa tca   5472
Lys Val     Cys Ser Trp Met Gly Cys Ile Tyr Met Gly Lys Gln Ser
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Cys Lys Tyr Lys Asn Lys Phe Asn Ser Tyr Trp Cys Ile His Asn Thr
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ttt ttt ttt tta ata atg ttt tat act tta gac cat taa ata tat tgt   5568
Phe Phe Phe Leu Ile Met Phe Tyr Thr Leu Asp His     Ile Tyr Cys
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gtg ata tgg ttt gac ccg tca gga ctc tct taa aaa gaa tga gta tct   5616
Val Ile Trp Phe Asp Pro Ser Gly Leu Ser     Lys Glu     Val Ser
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cgg aga ata tac tgg aga act gat cac tca tga tga agc taa tga gcg   5664
Arg Arg Ile Tyr Trp Arg Thr Asp His Ser         Ser         Ala
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tgg gag aat aga aga tcg gat tgg ttc ttc cta cct ctt tac ctt gaa   5712
Trp Glu Asn Arg Arg Ser Asp Trp Phe Phe Leu Pro Leu Tyr Leu Glu
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tga tca ggt aac ttc aga ata att ttg aag taa cgt ttt aat cat tcg   5760
    Ser Gly Asn Phe Arg Ile Ile Leu Lys     Arg Phe Asn His Ser
1905                1910                1915                1920

cgg gtt aca cat cta ttc gaa tca aag taa cat tta ttt tac agc tcg   5808
Arg Val Thr His Leu Phe Glu Ser Lys     His Leu Phe Tyr Ser Ser
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aaa tcg atg ctc gcc gta aag gaa acg agt tca aat ttc tca atc act   5856
Lys Ser Met Leu Ala Val Lys Glu Thr Ser Ser Asn Phe Ser Ile Thr
            1940                1945                1950

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Gln Gln Asp Leu Thr Ala Thr Pro Arg Tyr     Ala Val Ile Leu Tyr
        1955                1960                1965

ctt gaa caa ata cta aca tta tac aaa caa aaa tac tta tgt tag ttt   5952
Leu Glu Gln Ile Leu Thr Leu Tyr Lys Gln Lys Tyr Leu Cys     Phe
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ctt tag tta aat cgt gta tca act tta ctc gtc gtt gat tgg ttt tca   6000
Leu     Leu Asn Arg Val Ser Thr Leu Leu Val Val Asp Trp Phe Ser
1985                1990                1995                2000

tat tga aga tat tcc aag aaa ctc aaa ctc att tta aat gat ttt ttc   6048
Tyr     Arg Tyr Ser Lys Lys Leu Lys Leu Ile Leu Asn Asp Phe Phe
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ttg tcg aga aaa ttt agg tta cga aaa ttt atg gtt tcg tgt gca gtt   6096
Leu Ser Arg Lys Phe Arg Leu Arg Lys Phe Met Val Ser Cys Ala Val
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Asp Asp Cys Glu Arg Arg Ser Glu Asp Trp Ser Ile Cys Gly Glu Ser
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aca tgc gga ttg gtc gcg tgg tcg aga acc tag aaa gac tgg tgc ttc   6240
Thr Cys Gly Leu Val Ala Trp Ser Arg Thr     Lys Asp Trp Cys Phe
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taa aag gtc taa gga agc ccg tcc agc tcg tta gtt ttt gat ctg agg   6288
    Lys Val     Gly Ser Pro Ser Ser Ser Leu Val Phe Asp Leu Arg
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Arg Ser Ser Asn Ser Ser Ser Pro Phe Phe Met Leu Trp Tyr Ile Asn
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        Cys Asn Ala Ile Leu Cys Tyr     Thr Lys Thr     Val Ser
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Val Leu Phe Val Leu Gly Cys Phe Val Cys Ile Ile Cys Val Leu Thr
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Phe Lys Val Phe Phe Leu Tyr Phe Asn Leu Lys Thr Met Phe Met Leu
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Leu Val Cys Ile Asp Leu Trp Lys Lys Lys Ala Leu His Asn Phe Thr
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ttt att tag tct tca ttt agc gaa aaa tca cat aac aca agt ctg tgg   6576
Phe Ile     Ser Ser Phe Ser Glu Lys Ser His Asn Thr Ser Leu Trp
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tac gta atg tac aaa aat gtc aaa ata atg ggt ttt atc att aaa aaa   6624
Tyr Val Met Tyr Lys Asn Val Lys Ile Met Gly Phe Ile Ile Lys Lys
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aaa tat tgg tta tga atg aag tat agt tag aat ttt agg tat tag ctc   6672
Lys Tyr Trp Leu     Met Lys Tyr Ser     Asn Phe Arg Tyr     Leu
   2210                2215                2220

gtt tgg ttt taa aac gtt ttt cga gat tta att ttg tag tct att gag   6720
Val Trp Phe     Asn Val Phe Arg Asp Leu Ile Leu     Ser Ile Glu
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taa tac atg gaa gaa tca tca aca aag tgg ctg tag ctt acg aaa ggt   6768
    Tyr Met Glu Glu Ser Ser Thr Lys Trp Leu     Leu Thr Lys Gly
                2245                2250                2255

ttt act tta atg taa ata tgt att tga tgc atc taa cat tta gta tct   6816
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Ile Lys Arg Thr Met Ser Thr Thr Met Ser Ile Asn Pro Asp Lys Asn
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Leu Phe Leu Ala Thr His Glu Arg Trp Met Leu Val Arg Val Leu Phe
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Phe Leu Gly Leu His Glu Val Met Leu Met Trp Phe Arg Val Val Val
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Lys Pro Val Val Asp Asn Thr Ile Tyr Gly Val Tyr Val Glu Glu Arg
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Ile

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Leu

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Ser

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Gly Thr Leu Gly Glu Thr Pro Val Gln Ile Gln Cys Lys Asn Met Gln
35 40 45

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Lys Ile
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Leu Ile Met Phe Tyr Thr Leu Asp His
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Tyr Leu Cys

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Arg Arg
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Phe Thr Phe Ile
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Leu

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Arg

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Phe His Val Ser Leu Ser Ile Pro Pro Gln Leu Arg Ser Pro Ser Pro
20 25 30

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Ser Cys Phe Ser Ser Ser Ser Ser Leu
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Gly Ser Lys Glu Pro
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Val Trp Arg Val Ser Ile Leu
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Leu Glu Cys Phe
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Leu Leu Asn Gln Val Val Thr
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Phe Glu Asn
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His Tyr Pro Phe His Gln His Gln Arg Arg Arg Glu Lys Lys Lys Arg
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<400> 144
Ile Cys Leu Gly Lys Pro
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Tyr Ser Leu Leu Tyr Val Phe Leu Lys Ile Lys Glu Arg Arg Gly Leu
35 40 45

Asn Leu Ile Thr Ile Arg Phe Gln Arg Asp Val Lys Ile His Leu Ile
50 55 60

Asn Ser Tyr Thr Leu Val Ile Ile Phe Lys Thr Lys Lys Arg Asn Phe
65 70 75 80

Gln Thr Phe Lys Leu Lys Thr Glu Phe Arg Lys Cys Gln Arg Ile Asp
85 90 95

Asn Asp Ile Gln Ile Cys Arg Val Ser Lys Thr
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Tyr Lys Glu Thr Lys
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Cys Ile Tyr Gln Glu Ile Glu Ile Lys Thr Phe Val Phe Lys Tyr Ser
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Ser Phe Thr Ile Tyr Arg Val Gln Phe Leu Lys Phe Lys Lys Ser Phe
20 25 30

Thr Tyr Ile Leu Leu Asp
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Gln Arg Lys Phe Glu Leu Arg Tyr Ile Pro Ser Val Ala Thr His Ala
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Ser His His Gln Ser Phe Asp Leu Asn Gln Pro Ala Ala Glu Asp Asp
20 25 30

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Asn Gly Gly Asp Asn Lys Ser Leu Leu Ser Arg Met Gln Asn Pro Leu
         35                  40                  45

Arg His Phe Ser Ala Ser Ser Asp Tyr Asn Ser Tyr Glu Asp Gln Gly
      50                  55                  60

Tyr Val Leu Asp Glu Asp Gln Asp Tyr Ala Leu Glu Glu Asp Val Pro
 65                  70                  75                  80

Leu Phe Leu Asp Glu Asp Val Pro Leu Leu Pro Ser Val Lys Leu Pro
                 85                  90                  95

Ile Val Glu Lys Leu Pro Arg Ser Ile Thr Trp Val Phe Thr Lys Arg
            100                 105                 110

His Val Cys Phe Leu Phe Arg Thr Ser Phe Lys Ile Leu Ile Ile Tyr
        115                 120                 125

Tyr Ile Val Ile Thr His Ser Ala Tyr Ile His Phe Phe Asn Ile Ala
    130                 135                 140

Val Ala Ser
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Leu Val Arg Asp Lys Ser Ile Ile
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Met Val Arg His
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Arg Lys Lys Asn Ala Asn Phe Leu Lys Met
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Thr Asp Leu Tyr Gly
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<400> 157
Phe Leu His Tyr Ile Cys Ser
1 5

<210> 158
<211> 25
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Leu Leu Ile Cys Ser Pro Tyr Leu Ile Asn Cys Ser Arg Asn Phe Gln
1 5 10 15

Asp Gly Trp Ala Gly Leu Trp Phe Gly
20 25

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Ser Gly Arg Ala Ala Cys Ser Arg Gln Val Pro Arg Ser Gly Cys Phe
1 5 10 15

Gly His Ile Gly Asn Asn Ile Arg Ile Lys Thr Ser Tyr Val Asp Gln
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Trp Asn Cys Trp
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Phe Asp Ile Gln Asp Asn Asn Tyr Cys Phe Pro Gly Phe Cys
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<210> 164
<211> 59
<212> PRT
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1 5 10 15

Leu Ala Thr Lys Lys Gly Asp Asp His Thr Cys Phe Tyr Phe Ile Leu
20 25 30

Ser Phe Val Leu Gln Ile Phe Asp Cys His Met His Glu Lys Tyr Glu
35 40 45

Pro Glu Ser Arg Ser Val Ser Ile Lys Phe Ile
50 55

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Ile Ile Leu Leu Val Ser Gln Pro Leu Tyr Ile Arg Leu Ser Asp
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<211> 56
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<400> 166
Ile Ala Leu Ala Cys Gln Ser Glu Asp Lys Ser Ser Leu Phe Glu Asp
1 5 10 15

Glu Asp Arg Gln Pro Cys Ser Glu His Cys Tyr Leu Lys Val Ser Ile
20 25 30

Ser Leu Pro Leu Ser Leu Asn Phe Phe Val Tyr Ser Leu Ile Thr Phe
35 40 45

Ile Ser Tyr Trp Phe Asn Ile Lys
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<400> 167
Val Arg Ser Val Thr Glu Ala Asp His Val Met Asp Asn Asp Asn Ser
1 5 10 15

Ile Ser Asn Lys Ile Val Val Ser Asp Pro Asn Asn Thr Met Trp Thr
20 25 30

Pro Val Glu Lys Asp Leu Tyr Leu Lys Gly Ile Glu Ile Phe Gly Arg
35 40 45

Asn Arg
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<400> 168
Lys Asn Lys Asn Arg Phe Asn Ala Leu Ile Tyr Ile Leu Thr Leu Tyr
1 5 10 15

Ser Leu Ile Met Leu Val Arg Ser Cys Asp Val Ala Leu Asn Ile Leu
20 25 30

Arg Gly Leu Lys Thr Cys Leu Glu Ile Tyr Asn Tyr Met Arg Glu Gln
35 40 45

Asp Gln Cys Thr Met Ser Leu Asp Leu Asn Lys Thr Thr Gln Arg His
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Asn Gln Val His
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Lys His Met Lys Phe Pro Ile Cys Val Asp Gly Phe Ile Thr Gly Tyr
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Gln Lys Ser Ile Ser Lys Lys
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Cys Phe Lys Glu Asn Asn
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<211> 41
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Ser Ile Phe Pro Lys Pro Glu Asp Pro
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Glu Asp Val Ile Val Gln Leu Ala Asn Ala Gln Ile Asp Asn Val Leu
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Val Leu Leu Leu Ile Val Asn Ala Ile Gln Ile Phe Val Gly Val Val
35 40 45

Leu Leu Gly Asn Thr Phe Thr Ser Ile Ser Leu Tyr Thr Asn Ser Ile
50 55 60

Ile Lys Val Ile Gln Thr Lys Ser Leu Ile Lys Lys Thr Leu Tyr Ile
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85 90 95

Arg Thr Cys Asn Ser Ser Phe Lys Pro Ile Lys Arg
100 105

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<400> 173
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Ile

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<400> 174
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<210> 175
<211> 39
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<400> 175
Ile Leu Ile Gly Lys Ser Asp Val His Gly Trp Gly Ala Phe Thr Trp
1 5 10 15

Val Ser Asn His Val Asn Ile Arg Ile Ser Leu Ile Val Ile Gly Ala
20 25 30

Phe Ile Thr Leu Phe Phe Phe
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Cys Phe Ile Leu
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<400> 177
Thr Ile Lys Tyr Ile Val
1 5

<210> 178
<211> 53
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<400> 178
Tyr Gly Leu Thr Arg Gln Asp Ser Leu Lys Lys Asn Glu Tyr Leu Gly
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Glu Tyr Thr Gly Glu Leu Ile Thr His Asp Glu Ala Asn Glu Arg Gly
20 25 30

Arg Ile Glu Asp Arg Ile Gly Ser Ser Tyr Leu Phe Thr Leu Asn Asp
35 40 45

Gln Val Thr Ser Glu
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1 5 10 15

Asn Ile Tyr Phe Thr Ala Arg Asn Arg Cys Ser Pro
20 25

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<400> 180
Arg Lys Arg Val Gln Ile Ser Gln Ser Leu Ser Lys Thr
1 5 10

<210> 181
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<400> 181
Leu Leu Arg Gln Gly Thr Lys Pro Leu Tyr Phe Ile Leu Asn Lys Tyr
1 5 10 15

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His Tyr Thr Asn Lys Asn Thr Tyr Val Ser Phe Phe Ser
1 5 10

<210> 183
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<400> 183
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1 5 10 15

Ile Pro Arg Asn Ser Asn Ser Phe
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<211> 78
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<400> 184
Met Ile Phe Ser Cys Arg Glu Asn Leu Gly Tyr Glu Asn Leu Trp Phe
1 5 10 15

Arg Val Gln Leu Met Ile Val Arg Gly Asp Gln Arg Ile Gly Leu Phe
20 25 30

Ala Glu Arg Ala Ile Glu Glu Gly Glu Glu Leu Phe Phe Asp Tyr Cys
35 40 45

Tyr Gly Pro Glu His Ala Asp Trp Ser Arg Gly Arg Glu Pro Arg Lys
50 55 60

Thr Gly Ala Ser Lys Arg Ser Lys Glu Ala Arg Pro Ala Arg
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<400> 185
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20 25 30

Leu Phe Tyr Leu Phe
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<400> 186
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1 5

<210> 187
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<400> 187
Leu Ser Lys Phe Ser Phe Cys Ile Ser Ile
1 5 10

<210> 188
<211> 6
<212> PRT
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<400> 188
Lys Gln Cys Leu Cys Cys
1 5

<210> 189
<211> 29
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<400> 189
Thr Phe Gly Lys Lys Lys Leu Cys Thr Thr Leu His Leu Phe Ser Leu
1 5 10 15

His Leu Ala Lys Asn His Ile Thr Gln Val Cys Gly Thr
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<400> 190
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Phe Glu Ile

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Cys Ser Leu Arg Lys Val Leu Leu
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<400> 195
Tyr Leu Asn Lys
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<210> 196
<211> 13
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<400> 196
Lys Gln Lys Lys Arg Lys Lys Leu Phe Lys Ile Arg Lys
1 5 10

<210> 197
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<212> PRT
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<400> 197
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1 5 10 15

Thr Thr Ile Ala Lys Tyr Lys Cys
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<400> 198
Ile Tyr Met Lys Met
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<210> 199
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<400> 199
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<400> 201
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<210> 202
<211> 48
<212> PRT
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<400> 202
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Thr Arg Arg Leu Ser Ile Cys Arg Leu Cys Ser Ser Val Asn Leu Tyr
20 25 30

Phe Lys Thr Gly Gly Leu Phe Ile Thr Ile Ser Leu Asp Met Phe Leu
35 40 45

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Cys Arg Pro Lys Asn Arg Glu Ile Arg Lys Gly Thr Phe Val Val Ile
1 5 10 15

Val Thr Lys Gln Lys Ser Leu Tyr
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<400> 204
Ile Ile Arg Lys Asp Glu Lys Ile Lys Pro Leu
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<210> 205
<211> 12
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<400> 205
Leu Asp Asp His Arg Arg Gly Cys Gln Leu Gln Ser
1 5 10

<210> 206
<211> 34
<212> PRT
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<400> 206
Cys Phe Tyr Ile Asp Leu Ser Tyr Ile Leu Cys Ser Phe Thr Phe Lys
1 5 10 15

Lys Gln Tyr His Pro Ile Phe Phe Leu Leu Leu Ser Val Ser Ile Phe
20 25 30

Ala Asn

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<212> PRT
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<400> 207
Arg Asn Thr Lys Glu His Lys Lys Gln Leu Val Pro Asp Ser Thr Ile
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Ser Asn Asp Leu His
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<210> 208
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<212> PRT
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<400> 208
Pro Pro Pro Pro Ser Ile Phe Pro Leu Ser Phe Thr Ser Leu Ser Leu
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Tyr Leu Leu Asn Ser Gly His Arg Leu Arg Arg Phe Leu Cys Tyr Ser
20 25 30

Pro Gly Arg Cys Arg Ser Leu Ile His Asp Leu Val Ser His His Arg
35 40 45

Leu His Phe Asn Pro Gln Ser Leu Arg Lys Thr Arg Met Leu Cys Ser
50 55 60

Pro Phe Pro Ser Leu His Leu Leu Asp Arg Ser Leu His Arg Pro Ser
65 70 75 80

Leu Cys Leu Trp Asp Gln Lys Asn His Glu His Asp His Val Tyr Lys
85 90 95

Ser Arg Gln Lys Leu Val Ser Cys Asp Thr
100 105

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<213> Arabidopsis sp.

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Lys Met Asp Val Gly
1 5

<210> 210
<211> 15
<212> PRT
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<400> 210
Gly Phe Val Leu Phe Gly Ala Thr Arg Ser Asp Ala Asp Val Val
1 5 10 15

<210> 211
<211> 32
<212> PRT
<213> Arabidopsis sp.

<400> 211
Gln His Tyr Ile Trp Gly Leu Arg Gly Gly Glu Val Val Arg Glu Ser
1 5 10 15

Arg Cys Gly Ser Asp Leu Trp Tyr Asn Val Val Val Glu Ala Lys Arg
20 25 30

<210> 212
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<400> 212
Gly Arg Lys Ser Cys Gly Gly Gly Tyr Gly Gly
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<210> 213
<211> 42
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<400> 213
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Leu His Leu Cys Trp Asn Trp Phe Asn Glu Asp Leu Gln Arg Val Phe
20 25 30

Gly Phe Cys Glu Tyr Val Asp Phe Glu His
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Glu Val Glu Lys Arg Leu
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<212> PRT
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Ile Met Cys Phe
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<211> 27
<212> PRT
<213> Arabidopsis sp.

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Ser Cys Val Arg Tyr Leu Thr Tyr Tyr Thr His Leu Leu Asn Val Phe
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Glu Ile Phe Leu Phe Leu Phe Ser Ile Ser Cys
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Glu Phe Asn Pro Tyr Ile Cys His Lys Asn Ser Arg Ile Ser Glu Ser
1 5 10 15

Lys Asn Ile Leu Ser Lys Asn Asn His
20 25

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<210> 219
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Lys Ile Ser Asp Leu Arg Arg Ser Phe Lys Cys Val
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<210> 220
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Leu Asn Leu Arg Ile Glu
1 5

<210> 221
<211> 25
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Tyr Ser His Ile Tyr Ile Phe Glu Asp Leu Asn Ser Phe Cys Phe Phe
1 5 10 15

His Ile Cys Ile Ile Tyr Lys Leu Lys
20 25

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<400> 222
Ile Leu Ile Tyr Ile Met Thr Leu Ile
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Val Leu Pro Asp Thr Pro Lys Cys Ile Tyr
1 5 10

<210> 224
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<400> 224
Ser Ile Asn Ile Phe Ser Leu Val Tyr
1 5

<210> 225
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Thr Lys Leu Ser His Lys Tyr Glu Leu Thr Pro Phe Phe Leu
1 5 10

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Ala Val Lys Arg Gln Ala Asn Pro Thr Ser Thr Tyr Ile
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<400> 256
Thr Ala Gln Glu Ile Phe Arg Thr Val Gly Gln Asp Tyr Gly Leu Asp
1 5 10 15

Asp Leu Val Val Arg Arg Ala Leu Ala Lys Tyr Leu Glu Val Asp Val
20 25 30

Ser Asp Ile Leu Val Thr Ile Phe Glu
35 40

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<211> 30
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<400> 257
Lys Leu His Thr Ser Ile Asn Asn Phe Pro Ala Tyr Leu Ile Phe Val
1 5 10 15

Val Phe Arg Arg Glu Lys Cys Phe Lys Phe Ser Asn Leu Met
20 25 30

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<211> 51
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<400> 258
Glu Arg Tyr Asn Glu Leu Lys Leu Lys Asn Asp Gly Thr Ala Gly Glu
1 5 10 15

Ala Ser Asp Leu Thr Ser Lys Thr Ile Thr Thr Ala Phe Gln Asp Phe
20 25 30

Ala Asp Arg Arg His Cys Arg Arg Cys Met Val Thr Leu Asn Leu Ser
35 40 45

Phe Leu Ile
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<212> PRT
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<400> 259
Pro Gln Lys Arg Glu Met Ile Ile His Val Phe Ile Leu Phe Tyr His
1 5 10 15

Leu Phe Tyr Arg Tyr Ser Ile Val Ile Cys Met Arg Ser Met Ser Pro
20 25 30

Ser Leu Asp Pro
35

<210> 260
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<400> 260
Ala Leu Asn Ser Phe Lys Leu Phe Cys
1 5

<210> 261
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<400> 261
Phe His Asn Pro Tyr Ile
1 5

<210> 262
<211> 50
<212> PRT
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<400> 262
Val Ile Asn Leu Ile Arg Leu Leu Trp Leu Val Arg Ala Lys Thr Asn
1 5 10 15

Leu Val Cys Leu Arg Met Lys Ile Asp Asn His Ala Val Ser Ile Val
20 25 30

Thr Ser Arg Ser Leu Ser Leu Ser Leu Ser Leu Ser Ile Phe Leu Ser
35 40 45

Ile Pro
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Leu Arg Leu Leu Val Thr Gly Leu Ile Leu Asn Arg
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Gln Lys Leu Ile Met
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<210> 265
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Thr Thr Leu Cys Gly Arg Leu
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<400> 266
Arg Arg Ile Phe Thr
1 5

<210> 267
<211> 19
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<400> 267
Lys Glu Leu Arg Tyr Leu Gly Glu Thr Gly Lys Lys Ile Lys Ile Asp
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Leu Met His

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Tyr Ile Tyr Leu His Cys Ile Pro
1 5

<210> 269
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Leu Cys Trp Phe Ala Val Val Met Leu His
1 5 10

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Thr Tyr Phe Gly Gly Leu Arg Arg Ala
1 5

<210> 271
<211> 15
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<400> 271
Arg Phe Thr Ile Thr Cys Ala Asn Lys Ile Asn Val Leu Cys His
1 5 10 15

<210> 272
<211> 28
<212> PRT
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<400> 272
Thr Leu Thr Lys Leu His Lys Asp Thr Ile Arg Tyr Thr Asn Leu Cys
1 5 10 15

Arg Asn Tyr Ser His Asp Met Tyr Val Lys Asn Thr
20 25

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<211> 95
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<400> 273
Ser Phe Leu Tyr Val Leu Met Val Leu Ser Gln Val Thr Lys Lys Val
1 5 10 15

Ser Arg Lys Ser Ser Arg Ser Val Arg Lys Lys Ser Arg Leu Arg Lys
20 25 30

Tyr Ala Arg Tyr Pro Pro Ala Leu Lys Lys Thr Thr Ser Gly Glu Ala
35 40 45

Lys Phe Tyr Lys His Tyr Thr Pro Cys Thr Cys Lys Ser Lys Cys Gly
50 55 60

Gln Gln Cys Pro Cys Leu Thr His Glu Asn Cys Cys Glu Lys Tyr Cys
65 70 75 80

Gly Tyr Val Ile Gln Phe Phe Leu Ser Arg Lys Ile His Glu Ile
85 90 95

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Gln Ser Leu Trp Arg Met
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<400> 275
Leu Cys Asn Trp Pro Met His Lys Ser Thr Met Ser Leu Phe Cys Cys
1 5 10 15

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Met Arg Ser Arg Ser Leu Ser Glu Leu Ser Ser
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Val Thr Leu Ser Leu Gln Tyr Leu Phe Ile Gln Ile Leu
1 5 10

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Phe Lys Pro Lys Val Leu
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<400> 279
Lys Lys Leu Tyr Ile
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<400> 280
Leu Trp Arg Trp His Ser Trp
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<210> 281
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<400> 281
Asp Thr Ser Ala Asn Pro Met Gln Glu His Ala Ile Pro Pro Ser Asn
1 5 10 15

Gln

<210> 282
<211> 45
<212> PRT
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<400> 282
Lys Gly Asn Gln Arg Gln Ile Arg Thr Glu Asn Leu Lys Leu Ile Ile
1 5 10 15

Arg Lys Thr Phe Asn Tyr His Phe Pro Tyr Phe Thr Arg Phe Ser Leu
20 25 30

Glu Ser Leu Met Phe Met Asp Gly Val His Leu His Gly
35 40 45

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Leu Leu Val His Ser
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Leu Cys Asp Met Val
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Glu Asn

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Ser Phe Ala Gly Tyr Thr Ser Ile Arg Ile Lys Val Thr Phe Ile Leu
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Gln Leu Glu Ile Asp Ala Arg Arg Lys Gly Asn Glu Phe Lys Phe Leu
20 25 30

Asn His Ser Ala Arg Pro Asn Cys Tyr Ala Lys Val Leu Ser Arg Tyr
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Thr Leu Ser
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Val Lys Ser Cys Ile Asn Phe Thr Arg Arg
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Leu Val Phe Ile Leu Lys Ile Phe Gln Glu Thr Gln Thr His Phe Lys
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Phe Phe Leu Val Glu Lys Ile
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Val Thr Lys Ile Tyr Gly Phe Val Cys Ser
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Glu Glu Ile Arg Gly Leu Val Tyr Leu Arg Arg Glu Gln Ser Lys Lys
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Val Arg Ser Phe Ser Ser Thr Thr Ala Met Asp Gln Asn Met Arg Ile
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Gly Arg Val Val Glu Asn Leu Glu Arg Leu Val Leu Leu Lys Gly Leu
35 40 45

Arg Lys Pro Val Gln Leu Val Ser Phe
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Ser Glu Glu Lys Gln Gln Phe Lys Gln Ser Phe Phe Tyr Val Met Val
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Tyr Gln Leu Ile Met
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<400> 296
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Phe Arg Val Phe Cys Leu Tyr His Met Cys Leu Asn Phe Gln Ser Phe
20 25 30

Leu Phe Val Phe Gln Phe Lys Asn Asn Val Tyr Val Val Ser Leu His
35 40 45

Arg Pro Leu Glu Lys Lys Ser Phe Ala Gln Leu Tyr Ile Tyr Leu Val
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Phe Ile
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Arg Lys Ile Thr
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<211> 18
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Tyr His

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<400> 299
Lys Lys Ile Leu Val Met Asn Glu Val
1 5

<210> 300
<211> 18
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Val Leu Ala Arg Leu Val Leu Lys Arg Phe Ser Arg Phe Asn Phe Val
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Val Tyr

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<400> 301
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Phe Tyr Phe Asn Val Asn Met Tyr Leu Met His Leu Thr Phe Ser Ile
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<211> 22
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1 5 10 15

Asn Tyr Phe Gln Lys Ile
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<210> 303
<211> 21
<212> PRT
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<400> 303
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Asn Ala Lys Tyr Thr
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<400> 304
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Lys Trp Arg Asp
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Cla-73

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<210> 315
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